

Genforce version 5.1.3  
Copyright (C) 1993 - 2003 CompuGen Ltd.  
OK protein - nucleic search, using frame\_plus\_pn model  
Run on: January 6, 2003, 15:22:35 : Search time 2415 seconds  
5005.966 Million cell updates/sec

Seq14-JOIN-SEQ4  
Sequence: 2250

Scoring table: BLASTN2  
Sequence: 1 NPVIVDVCYIPPHRVS.....PKVDSCKSTKPVCHRS 432

Searched: 2054640 seps, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODES=frames\_p2n\_model

-DB=GenBank1

-OPT=fastp

-SUFFIX=rge

-MINMATCH=0

-LOOPT=0

-XGAPEXT=0

-UNITS=bits

-START=1

-END=1

-MATRIX=blosum62

-TRANS=human40.cdi

-LIST=45

-OPTMT=pclo

-NORMALIZE=HEAPSIZE=500

-MINLEN=2000000000

-USER=MEZMAIN0877476

-RCGN=1

-2827

-RUN=0612003124916\_21

-MCPU=6

-ICPU=3

-MARK\_THRESHOLD=30

-THREADS=1

-XGAPOP=10

-XGAPEXT=0.5

-YGAPOP=6

-YGAEXT=7

Database :

1: gb\_ba.\*

2: gb\_ba.\*

3: gb\_ba.\*

4: gb\_ba.\*

5: gb\_ba.\*

6: gb\_ba.\*

7: gb\_ba.\*

8: gb\_ba.\*

9: gb\_ba.\*

10: gb\_ba.\*

11: gb\_ba.\*

12: gb\_ba.\*

13: gb\_ba.\*

14: gb\_ba.\*

15: gb\_ba.\*

16: gb\_ba.\*

17: gb\_ba.\*

18: gb\_ba.\*

19: gb\_ba.\*

20: gb\_ba.\*

21: gb\_ba.\*

22: gb\_ba.\*

23: gb\_ba.\*

24: gb\_ba.\*

25: gb\_ba.\*

26: gb\_ba.\*

27: gb\_ba.\*

28: gb\_ba.\*

Prod. No. is the number of results predicted by chance to have a  
score as high as the observed score. Results are being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query	Length	DB	ID	Description
1	244	99.7	1521	6	AX358169	Sequence
2	240	99.6	1521	6	AX358170	Sequence
3	240	99.6	1521	6	AX358171	Sequence
4	237	99.4	1521	6	AX358163	Sequence
5	237	99.4	1521	6	AX358164	Sequence
6	233	99.2	1521	6	AX358175	Sequence
7	2198	93.7	1518	6	AX358165	Sequence
8	2198	93.7	1518	6	AX358159	Sequence
9	2198	93.7	1518	6	AX358159	Sequence
10	2191	93.4	1518	6	AX358173	Sequence
11	2191	93.4	1518	6	AX358169	Sequence
12	2191	93.4	1518	6	AX358169	Sequence
13	2191	93.4	1518	6	AX358169	Sequence
14	2191	93.4	1518	6	AX358169	Sequence
15	2191	93.4	1518	6	AX358169	Sequence
16	2191	93.4	1518	6	AX358169	Sequence
17	2191	93.4	1518	6	AX358169	Sequence
18	2191	93.4	1518	6	AX358169	Sequence
19	2191	93.4	1518	6	AX358169	Sequence
20	2191	93.4	1518	6	AX358169	Sequence
21	2191	93.4	1518	6	AX358169	Sequence
22	2191	93.4	1518	6	AX358169	Sequence
23	2191	93.4	1518	6	AX358169	Sequence
24	2191	93.4	1518	6	AX358169	Sequence
25	2191	93.4	1518	6	AX358169	Sequence
26	2191	93.4	1518	6	AX358169	Sequence
27	2191	93.4	1518	6	AX358169	Sequence
28	2191	93.4	1518	6	AX358169	Sequence
29	2191	93.4	1518	6	AX358169	Sequence
30	2191	93.4	1518	6	AX358169	Sequence
31	2191	93.4	1518	6	AX358169	Sequence
32	2191	93.4	1518	6	AX358169	Sequence
33	2191	93.4	1518	6	AX358169	Sequence
34	2191	93.4	1518	6	AX358169	Sequence
35	2191	93.4	1518	6	AX358169	Sequence
36	2191	93.4	1518	6	AX358169	Sequence
37	2191	93.4	1518	6	AX358169	Sequence
38	2191	93.4	1518	6	AX358169	Sequence
39	2191	93.4	1518	6	AX358169	Sequence
40	2191	93.4	1518	6	AX358169	Sequence
41	2191	93.4	1518	6	AX358169	Sequence
42	2191	93.4	1518	6	AX358169	Sequence
43	2191	93.4	1518	6	AX358169	Sequence
44	2191	93.4	1518	6	AX358169	Sequence
45	2191	93.4	1518	6	AX358169	Sequence

## ALIGNMENTS

RESULT 1





















[illegible]





















```

Db 781 ATGTGCTGCTAGTACGACACTATGCGGTGTGTCTCTGACGACGATATCTAC 840
Oy 182 AantTeyrAlaLyspAenAgsrMetwetaLSerAnysyLLeuPhaAgly 201
Db 841 ATGTTGATTTTGTATGACAGAGAGAGATGATACACCACTCTCTCTGATGAT 900
Oy 202 ATGTTGATTTTGTATGACAGAGAGAGATGATACACCACTCTCTCTGATGAT 900
Db 901 GCTCTGCGGTTTCTATACAGATATGATGAGAGAGAGAGAGAGAGAGAGAG 960
Oy 222 ValLethwAlaLyspAenAgsrMetwetaLSerAnysyLLeuPhaAgly 241
Db 961 GTATCATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Oy 242 GATCATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 1021 GATCATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Oy 262 GATCATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1081 GATCATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Oy 282 LysCysPheLysPheLysPheLysPheLysPheLysPheLysPheLys 301
Db 1141 GATCATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Oy 321 TyrTyrPheLysPheLysPheLysPheLysPheLysPheLysPheLys 341
Db 1258 GCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1317
Oy 362 TyrTyrPheLysPheLysPheLysPheLysPheLysPheLysPheLys 381
Db 1318 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1377
Oy 392 TyrTyrPheLysPheLysPheLysPheLysPheLysPheLysPheLys 411
Db 1378 TACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1437
Oy 382 LysCysPheLysPheLysPheLysPheLysPheLysPheLysPheLys 401
Db 1438 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1497
Oy 402 AnserProLysCysLysPheLysPheLysPheLysPheLysPheLys 416
Db 1498 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1542

```

## RESULT 5

US-08-568-373-3

Sequence 3, Application US/0868373

Patent No. 307118

APPLICANT: Jansco, Jan G.

APPLICANT: Post-Bettlemiller, Martha A.

TITLE OF INVENTION: PART ACID ELONGASES

FILE REFERENCE: 07146/064001

CURRENT FILING DATE: 1997-06-03

NUMBER OF SEQ. ID NOS: 22

SOFTWARE: FASTSEQ for Windows version 3.0

SEQUENCE LENGTH: 1479

TYPE: DNA

SOURCE: Anabidopsis thaliana

US-08-568-373-3

Alignment Scores:

Seq.:

Length:

Matches:

Score:

```

Percent Similarity: 81.63%
Query Match: 67.33%
Identical: 70
Gap: 3
Seq14-join-seq4 (1-432) x US-08-568-373-3 (1-1479)
Oy 2 PhvAlaLyspAenAgsrMetwetaLSerAnysyLLeuPhaAgly 21
Db 232 CCGTTTATGCTGCTAGCTACTGCTACGCGCGCGCGCGCGCGCGCGCG 291
Oy 232 SerLysPheLysPheLysPheLysPheLysPheLysPheLysPheLys 41
Db 292 CAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 345
Oy 42 TheCysPheLysPheLysPheLysPheLysPheLysPheLysPheLys 60
Db 346 -----GATCATGTGATGATGATGATGATGATGATGATGATGATG 396
Oy 61 LeuLysPheLysPheLysPheLysPheLysPheLysPheLysPheLys 80
Db 397 CTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 456
Oy 81 AlaAlaLyspAenAgsrMetwetaLSerAnysyLLeuPhaAgly 100
Db 457 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 516
Oy 101 Anabidopsis thaliana 120
Db 517 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 576
Oy 121 ProthPheLysPheLysPheLysPheLysPheLysPheLysPheLys 140
Db 577 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 636
Oy 141 SerPheLysPheLysPheLysPheLysPheLysPheLysPheLys 160
Db 637 AGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 696
Oy 161 AspLeuLysPheLysPheLysPheLysPheLysPheLysPheLysPheLys 180
Db 697 AGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 756
Oy 181 TyrAniLysPheLysPheLysPheLysPheLysPheLysPheLysPheLys 200
Db 757 CAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 816
Oy 201 GTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 220
Db 817 GGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 876
Oy 221 LeuAlaLyspAenAgsrMetwetaLSerAnysyLLeuPhaAgly 240
Db 877 CTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 936
Oy 241 GATCATGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 260
Db 937 CAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 296
Oy 261 AlaCysPheLysPheLysPheLysPheLysPheLysPheLysPheLys 280
Db 997 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1056
Oy 281 GATCATGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
Db 1057 GATCATGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1116
Oy 301 HisTyrPheLysPheLysPheLysPheLysPheLysPheLysPheLys 320
Db 1117 CAT-----TACATGATGATGATGATGATGATGATGATGATGATG 1173
Oy 321 Anabidopsis thaliana 340
Db 1173 -----TACATGATGATGATGATGATGATGATGATGATGATG 1233

```













Db	1479	TCAGGTTTCAGGTACACAGTGTCTGTGTGGAGGGGCTTTGAGGAGTGTCACATCCGCGTAGA	1538
Qy	401	ThrAnSerProFzPgiuHisCysIleAspArgTyrProvalIle	416
Db	1939	GAGAGAGATCTCTGGATGGATGAAATGAGAAGTCCCTCGTCATGTG	1986

RESULT 11  
US-08-926-522-21

1 Patent No. 6426447  
2       GRANTED: 1999-07-27  
3       CLASSIFICATION: G06F 07/00  
4       APPLICANT: VIG C. Knauf  
5       INVENTOR: GREGORY A. Thompson  
6       TITLE: METHOD FOR SETTING AND SENDING OILS  
7       NUMBER OF SEQUENCES: 23  
8       CORRESPONDENCE ADDRESS: INC.  
9       CITY: COVINGTON  
10       STREET: 1940 Fifth Street  
11       STATE: LOUISIANA















US-09-877-476-13

Alignment Scores: 1e-264 Length: 1521  
 Pred. No.: 2243,00 Matches: 431  
 Score Similarity: 99.77% Mismatches: 1  
 Best Local Similarity: 99.77% Indels: 0  
 Query Match: 99.73% Gaps: 0

SQ14-JOIN-SQ4 (1-432) x US-09-877-476-13 (1-1521)

Qy 1 AseProValrYveLauAapSerPheCyfTherProLisLeuAerValSer 20  
 Db 223 ANYCGGTTTATCTCGTGAAGTACTCTGTTACTCTCCGACGATCTCAGAGTTAT 1122  
 Qy 21 ValSerYveLauAapSerPheGlyIleLysValAapSerPheSerPhe 40  
 Db 283 GTCTCTAAGTCAAGAGATATTTCTACCAATPAAAGAAAGCTGATCTTACAGAAC 1242  
 Qy 41 GlyTherPheLauAapSerPheSerPheLysValAapSerPheSerPhe 60  
 Db 343 SGGACGGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1302  
 Qy 61 LeuAapSerPheLysValAapSerPheSerPheSerPheSerPheSerPhe 80  
 Db 1303 CTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1362  
 Qy 403 CTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1422  
 Qy 81 AAlaValAapSerPheGlyIleLysValAapSerPheSerPheSerPhe 100  
 Db 463 CG 1518  
 Qy 101 AseProValrYveLauAapSerPheCyfTherProLisLeuAerValSer 120  
 Db 523 AAGACACACGTTACCTTACGATATGATATGATATGATATGATATGATATGATATGAT 582  
 Qy 121 ProTherProSerLeuSerAlaMetValAapSerPheLysValAapSerPheVal 140  
 Db 583 CGACCTCTCGCTCTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 642  
 Qy 141 SerPheLauAapSerPheLysValAapSerPheLysValAapSerPheLys 160  
 Db 643 AGCTTAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 702  
 Qy 161 AseProValrYveLauAapSerPheCyfTherProLisLeuAerValSer 180  
 Db 703 GATCTGTGATCTCATTAATATGATATGATATGATATGATATGATATGATATGATATGAT 762  
 Qy 181 ProTherProSerLeuSerAlaMetValAapSerPheLysValAapSerPheVal 200  
 Db 763 TATACATCTTACCTGATGATATGATGATGATGATGATGATGATGATGATGATGATGAT 822  
 Qy 201 GlyTherPheLauAapSerPheLysValAapSerPheLysValAapSerPheLys 220  
 Db 823 GTGGCGCGCGCTATTTCTCTCCACACGCGCGATGATGATGATGATGATGATGATGAT 882  
 Qy 221 LeuAapSerPheLysValAapSerPheLysValAapSerPheLysValAapSer 240  
 Db 883 CTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 942  
 Qy 241 GILYDAPAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAP 960  
 Db 943 CAGGAC 1002  
 Qy 261 AILGIVGTHYVVALYVLAAMETVALAETHYVALAETHYVALAETHYVALAETHYVAL 280  
 Db 1003 GT 1062  
 Qy 281 GILYDAPAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAP 300  
 Db 1063 GAAAGAACT 1122  
 Qy 301 HATYTYTYVALYVLAAMETVALAETHYVALAETHYVALAETHYVALAETHYVAL 320

Db 1123 ATCTACTACTCTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1182  
 Qy 321 KVALPVALIATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 340  
 Db 1183 AGGCG 1242  
 Qy 341 SerAapSerPheLysValAapSerPheLysValAapSerPheLysValAapSer 360  
 Db 1243 AT 1302  
 Qy 361 AT 380  
 Db 1303 CTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1362  
 Qy 381 GILYDAPAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAP 400  
 Db 1363 GGGTCAAGCTCTTAAAGTGTACACATGATGATGATGATGATGATGATGATGATGATGAT 1422  
 Qy 401 TharSerProLisLeuAapSerPheLysValAapSerPheLysValAapSerPhe 420  
 Db 1423 ACAAATATCTCTGGACACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1482  
 Qy 421 GILYDAPAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAP 440  
 Db 1483 GTHATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1542  
 RESULT 2  
 US-09-877-476-21 Application US-09877476  
 GENERAL INFORMATION: Jan G.  
 PATENT NO. US20020049994A1  
 APPLICANT: BlackLock, Brenda J.  
 TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA  
 FILE REFERENCE: 07146-10000  
 CURRENT APPLICATION NUMBER: US/09/877,476  
 CURRENT FILING DATE: 2001-06-08/210,326  
 PRIOR FILING DATE: 2000-06-08  
 NUMBER OF SEQ ID NOS: 56  
 NUMBER OF SEQ ID NOS for Windows Version 4.0  
 SEQ ID NO 21  
 LENGTH: 1521  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: 5' 342 bp from A. thaliana FABI (SEQ ID NO:1) and  
 OTHER INFORMATION: NO:3) having mutations at positions 275 and 920;  
 OTHER INFORMATION: designated At114 K92R G307D; hypothetical  
 LOCATION: C13...((1518))  
 US-09-877-476-21  
 Alignment scores: 1.33e-264 Length: 1521  
 Pred. No.: 2243,00 Matches: 431  
 Score Similarity: 99.77% Mismatches: 1  
 Best Local Similarity: 99.77% Indels: 0  
 Query Match: 99.69% Gaps: 0

SQ14-JOIN-SQ4 (1-432) x US-09-877-476-21 (1-1521)

Qy 1 AseProValrYveLauAapSerPheCyfTherProLisLeuAerValSer 20  
 Db 223 ANYCGGTTTATCTCGTGAAGTACTCTGTTACTCTCCGACGATCTCAGAGTTAT 282  
 Qy 21 ValSerYveLauAapSerPheGlyIleLysValAapSerPheSerPhe 40  
 Db 283 GTCTCTAAGTCAAGAGATATTTCTACCAATPAAAGAAAGCTGATCTTACAGAAC 342



[illegible]

```

1  CURRENT FILING DATE: 2000-06-08
2  PRIOR FILING DATE: 2000-06-08
3  PRIOR FILING DATE: 2000-06-08
4  NUMBER OF SEQ ID NOS: 36
5  NUMBER OF SEQ ID NOS: 36
6  NUMBER OF SEQ ID NOS: 36
7  SEQ ID NO 1: SEQ ID NO 1
8  SEQ ID NO 2: SEQ ID NO 2
9  SEQ ID NO 3: SEQ ID NO 3
10 SEQ ID NO 4: SEQ ID NO 4
11 SEQ ID NO 5: SEQ ID NO 5
12 SEQ ID NO 6: SEQ ID NO 6
13 SEQ ID NO 7: SEQ ID NO 7
14 SEQ ID NO 8: SEQ ID NO 8
15 SEQ ID NO 9: SEQ ID NO 9
16 SEQ ID NO 10: SEQ ID NO 10
17 SEQ ID NO 11: SEQ ID NO 11
18 SEQ ID NO 12: SEQ ID NO 12
19 SEQ ID NO 13: SEQ ID NO 13
20 SEQ ID NO 14: SEQ ID NO 14
21 SEQ ID NO 15: SEQ ID NO 15
22 SEQ ID NO 16: SEQ ID NO 16
23 SEQ ID NO 17: SEQ ID NO 17
24 SEQ ID NO 18: SEQ ID NO 18
25 SEQ ID NO 19: SEQ ID NO 19
26 SEQ ID NO 20: SEQ ID NO 20
27 SEQ ID NO 21: SEQ ID NO 21
28 SEQ ID NO 22: SEQ ID NO 22
29 SEQ ID NO 23: SEQ ID NO 23
30 SEQ ID NO 24: SEQ ID NO 24
31 SEQ ID NO 25: SEQ ID NO 25
32 SEQ ID NO 26: SEQ ID NO 26
33 SEQ ID NO 27: SEQ ID NO 27
34 SEQ ID NO 28: SEQ ID NO 28
35 SEQ ID NO 29: SEQ ID NO 29
36 SEQ ID NO 30: SEQ ID NO 30
37 SEQ ID NO 31: SEQ ID NO 31
38 SEQ ID NO 32: SEQ ID NO 32
39 SEQ ID NO 33: SEQ ID NO 33
40 SEQ ID NO 34: SEQ ID NO 34
41 SEQ ID NO 35: SEQ ID NO 35
42 SEQ ID NO 36: SEQ ID NO 36
43 SEQ ID NO 37: SEQ ID NO 37
44 SEQ ID NO 38: SEQ ID NO 38
45 SEQ ID NO 39: SEQ ID NO 39
46 SEQ ID NO 40: SEQ ID NO 40
47 SEQ ID NO 41: SEQ ID NO 41
48 SEQ ID NO 42: SEQ ID NO 42
49 SEQ ID NO 43: SEQ ID NO 43
50 SEQ ID NO 44: SEQ ID NO 44
51 SEQ ID NO 45: SEQ ID NO 45
52 SEQ ID NO 46: SEQ ID NO 46
53 SEQ ID NO 47: SEQ ID NO 47
54 SEQ ID NO 48: SEQ ID NO 48
55 SEQ ID NO 49: SEQ ID NO 49
56 SEQ ID NO 50: SEQ ID NO 50
57 SEQ ID NO 51: SEQ ID NO 51
58 SEQ ID NO 52: SEQ ID NO 52
59 SEQ ID NO 53: SEQ ID NO 53
60 SEQ ID NO 54: SEQ ID NO 54
61 SEQ ID NO 55: SEQ ID NO 55
62 SEQ ID NO 56: SEQ ID NO 56
63 SEQ ID NO 57: SEQ ID NO 57
64 SEQ ID NO 58: SEQ ID NO 58
65 SEQ ID NO 59: SEQ ID NO 59
66 SEQ ID NO 60: SEQ ID NO 60
67 SEQ ID NO 61: SEQ ID NO 61
68 SEQ ID NO 62: SEQ ID NO 62
69 SEQ ID NO 63: SEQ ID NO 63
70 SEQ ID NO 64: SEQ ID NO 64
71 SEQ ID NO 65: SEQ ID NO 65
72 SEQ ID NO 66: SEQ ID NO 66
73 SEQ ID NO 67: SEQ ID NO 67
74 SEQ ID NO 68: SEQ ID NO 68
75 SEQ ID NO 69: SEQ ID NO 69
76 SEQ ID NO 70: SEQ ID NO 70
77 SEQ ID NO 71: SEQ ID NO 71
78 SEQ ID NO 72: SEQ ID NO 72
79 SEQ ID NO 73: SEQ ID NO 73
80 SEQ ID NO 74: SEQ ID NO 74
81 SEQ ID NO 75: SEQ ID NO 75
82 SEQ ID NO 76: SEQ ID NO 76
83 SEQ ID NO 77: SEQ ID NO 77
84 SEQ ID NO 78: SEQ ID NO 78
85 SEQ ID NO 79: SEQ ID NO 79
86 SEQ ID NO 80: SEQ ID NO 80
87 SEQ ID NO 81: SEQ ID NO 81
88 SEQ ID NO 82: SEQ ID NO 82
89 SEQ ID NO 83: SEQ ID NO 83
90 SEQ ID NO 84: SEQ ID NO 84
91 SEQ ID NO 85: SEQ ID NO 85
92 SEQ ID NO 86: SEQ ID NO 86
93 SEQ ID NO 87: SEQ ID NO 87
94 SEQ ID NO 88: SEQ ID NO 88
95 SEQ ID NO 89: SEQ ID NO 89
96 SEQ ID NO 90: SEQ ID NO 90
97 SEQ ID NO 91: SEQ ID NO 91
98 SEQ ID NO 92: SEQ ID NO 92
99 SEQ ID NO 93: SEQ ID NO 93
100 SEQ ID NO 94: SEQ ID NO 94
101 SEQ ID NO 95: SEQ ID NO 95
102 SEQ ID NO 96: SEQ ID NO 96
103 SEQ ID NO 97: SEQ ID NO 97
104 SEQ ID NO 98: SEQ ID NO 98
105 SEQ ID NO 99: SEQ ID NO 99
106 SEQ ID NO 100: SEQ ID NO 100
107 SEQ ID NO 101: SEQ ID NO 101
108 SEQ ID NO 102: SEQ ID NO 102
109 SEQ ID NO 103: SEQ ID NO 103
110 SEQ ID NO 104: SEQ ID NO 104
111 SEQ ID NO 105: SEQ ID NO 105
112 SEQ ID NO 106: SEQ ID NO 106
113 SEQ ID NO 107: SEQ ID NO 107
114 SEQ ID NO 108: SEQ ID NO 108
115 SEQ ID NO 109: SEQ ID NO 109
116 SEQ ID NO 110: SEQ ID NO 110
117 SEQ ID NO 111: SEQ ID NO 111
118 SEQ ID NO 112: SEQ ID NO 112
119 SEQ ID NO 113: SEQ ID NO 113
120 SEQ ID NO 114: SEQ ID NO 114
121 SEQ ID NO 115: SEQ ID NO 115
122 SEQ ID NO 116: SEQ ID NO 116
123 SEQ ID NO 117: SEQ ID NO 117
124 SEQ ID NO 118: SEQ ID NO 118
125 SEQ ID NO 119: SEQ ID NO 119
126 SEQ ID NO 120: SEQ ID NO 120
127 SEQ ID NO 121: SEQ ID NO 121
128 SEQ ID NO 122: SEQ ID NO 122
129 SEQ ID NO 123: SEQ ID NO 123
130 SEQ ID NO 124: SEQ ID NO 124
131 SEQ ID NO 125: SEQ ID NO 125
132 SEQ ID NO 126: SEQ ID NO 126
133 SEQ ID NO 127: SEQ ID NO 127
134 SEQ ID NO 128: SEQ ID NO 128
135 SEQ ID NO 129: SEQ ID NO 129
136 SEQ ID NO 130: SEQ ID NO 130
137 SEQ ID NO 131: SEQ ID NO 131
138 SEQ ID NO 132: SEQ ID NO 132
139 SEQ ID NO 133: SEQ ID NO 133
140 SEQ ID NO 134: SEQ ID NO 134
141 SEQ ID NO 135: SEQ ID NO 135
142 SEQ ID NO 136: SEQ ID NO 136
143 SEQ ID NO 137: SEQ ID NO 137
144 SEQ ID NO 138: SEQ ID NO 138
145 SEQ ID NO 139: SEQ ID NO 139
146 SEQ ID NO 140: SEQ ID NO 140
147 SEQ ID NO 141: SEQ ID NO 141
148 SEQ ID NO 142: SEQ ID NO 142
149 SEQ ID NO 143: SEQ ID NO 143
150 SEQ ID NO 144: SEQ ID NO 144
151 SEQ ID NO 145: SEQ ID NO 145
152 SEQ ID NO 146: SEQ ID NO 146
153 SEQ ID NO 147: SEQ ID NO 147
154 SEQ ID NO 148: SEQ ID NO 148
155 SEQ ID NO 149: SEQ ID NO 149
156 SEQ ID NO 150: SEQ ID NO 150
157 SEQ ID NO 151: SEQ ID NO 151
158 SEQ ID NO 152: SEQ ID NO 152
159 SEQ ID NO 153: SEQ ID NO 153
160 SEQ ID NO 154: SEQ ID NO 154
161 SEQ ID NO 155: SEQ ID NO 155
162 SEQ ID NO 156: SEQ ID NO 156
163 SEQ ID NO 157: SEQ ID NO 157
164 SEQ ID NO 158: SEQ ID NO 158
165 SEQ ID NO 159: SEQ ID NO 159
166 SEQ ID NO 160: SEQ ID NO 160
167 SEQ ID NO 161: SEQ ID NO 161
168 SEQ ID NO 162: SEQ ID NO 162
169 SEQ ID NO 163: SEQ ID NO 163
170 SEQ ID NO 164: SEQ ID NO 164
171 SEQ ID NO 165: SEQ ID NO 165
172 SEQ ID NO 166: SEQ ID NO 166
173 SEQ ID NO 167: SEQ ID NO 167
174 SEQ ID NO 168: SEQ ID NO 168
175 SEQ ID NO 169: SEQ ID NO 169
176 SEQ ID NO 170: SEQ ID NO 170
177 SEQ ID NO 171: SEQ ID NO 171
178 SEQ ID NO 172: SEQ ID NO 172
179 SEQ ID NO 173: SEQ ID NO 173
180 SEQ ID NO 174: SEQ ID NO 174
181 SEQ ID NO 175: SEQ ID NO 175
182 SEQ ID NO 176: SEQ ID NO 176
183 SEQ ID NO 177: SEQ ID NO 177
184 SEQ ID NO 178: SEQ ID NO 178
185 SEQ ID NO 179: SEQ ID NO 179
186 SEQ ID NO 180: SEQ ID NO 180
187 SEQ ID NO 181: SEQ ID NO 181
188 SEQ ID NO 182: SEQ ID NO 182
189 SEQ ID NO 183: SEQ ID NO 183
190 SEQ ID NO 184: SEQ ID NO 184
191 SEQ ID NO 185: SEQ ID NO 185
192 SEQ ID NO 186: SEQ ID NO 186
193 SEQ ID NO 187: SEQ ID NO 187
194 SEQ ID NO 188: SEQ ID NO 188
195 SEQ ID NO 189: SEQ ID NO 189
196 SEQ ID NO 190: SEQ ID NO 190
197 SEQ ID NO 191: SEQ ID NO 191
198 SEQ ID NO 192: SEQ ID NO 192
199 SEQ ID NO 193: SEQ ID NO 193
200 SEQ ID NO 194: SEQ ID NO 194
201 SEQ ID NO 195: SEQ ID NO 195
202 SEQ ID NO 196: SEQ ID NO 196
203 SEQ ID NO 197: SEQ ID NO 197
204 SEQ ID NO 198: SEQ ID NO 198
205 SEQ ID NO 199: SEQ ID NO 199
206 SEQ ID NO 200: SEQ ID NO 200
207 SEQ ID NO 201: SEQ ID NO 201
208 SEQ ID NO 202: SEQ ID NO 202
209 SEQ ID NO 203: SEQ ID NO 203
210 SEQ ID NO 204: SEQ ID NO 204
211 SEQ ID NO 205: SEQ ID NO 205
212 SEQ ID NO 206: SEQ ID NO 206
213 SEQ ID NO 207: SEQ ID NO 207
214 SEQ ID NO 208: SEQ ID NO 208
215 SEQ ID NO 209: SEQ ID NO 209
216 SEQ ID NO 210: SEQ ID NO 210
217 SEQ ID NO 211: SEQ ID NO 211
218 SEQ ID NO 212: SEQ ID NO 212
219 SEQ ID NO 213: SEQ ID NO 213
220 SEQ ID NO 214: SEQ ID NO 214
221 SEQ ID NO 215: SEQ ID NO 215
222 SEQ ID NO 216: SEQ ID NO 216
223 SEQ ID NO 217: SEQ ID NO 217
224 SEQ ID NO 218: SEQ ID NO 218
225 SEQ ID NO 219: SEQ ID NO 219
226 SEQ ID NO 220: SEQ ID NO 220
227 SEQ ID NO 221: SEQ ID NO 221
228 SEQ ID NO 222: SEQ ID NO 222
229 SEQ ID NO 223: SEQ ID NO 223
230 SEQ ID NO 224: SEQ ID NO 224
231 SEQ ID NO 225: SEQ ID NO 225
232 SEQ ID NO 226: SEQ ID NO 226
233 SEQ ID NO 227: SEQ ID
```

RESULT 4  
 US-09-877-476-7  
 : Sequence 7, Application US/09877476  
 : Patent No. US20020049594A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Javorzki, Jan G.  
 : APPLICANT: Blacklock, Brenda J.  
 : TITLE OF INVENTION: SYNTHASE FOURTEEN  
 : FILE REFERENCE: 07148-108001  
 : CURRENT APPLICATION NUMBER: US/877,476







; SOFTWARE: PatsSeq for Windows Version 4.0

; SEQ ID NO 1334

; TYPE: DNA

; ORGANISM: Brassica napus

; NAME: B. napus

; NAME/KEY: CDS

; LOCATION: (1)...(1321)

US-09-877-476-3

DB:

Alignment Scores:

Pred. No.: 3,73e-259

Length: 1524

Percent Similarity: 98.84

Best Local Similarity: 98.84

Query Match: 97.71%

Mismatches: 4

Indels: 1

Gaps: 10

SEQ14-JOIN-SEQ4 (1-432) x US-09-877-476-3 (1-1524)

Qy 2 ProvalityLeuValAspYSerCytTrpLeuProProlisLeuValGuaSerVal 21  
 Db 229 CCGGTTACTCTGAGTAACTGACATCTCTCCACACCGCATGATGATGATGATC 288  
 Qy 22 SerValValMetAspIlePheThrGluLeuValGuaSerValGuaSerVal 41  
 Db 289 TCGGAGTGGAGATGCTTTTATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 345  
 Qy 42 TheCyAAspPheSerTrpIleAspPheValGuaSerValGuaSerValGua 61  
 Db 346 AGCTGGAGTGGAGATGCTTTTATGAGTGAAGAGAGAGAGAGAGAGAGAGAG 405  
 Qy 62 GlAspGluValGluValGluValGluValGluValGluValGluValGluVal 81  
 Db 406 GCGGATGAAATCACGGGCGCCAGGGGGTCTTCAAGTCTCTCCCGGAGAGAT 465  
 Qy 82 AAlaAlaGluGluThrGluGluValLeuLeuLeuLeuLeuLeuLeuLeuLeu 101  
 Db 466 CCGGCGCGCTGAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 525  
 Qy 102 TheAAspValMetAspIleGluValGuaSerValGuaSerValGuaSerVal 121  
 Db 526 ACCGAGTAACTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 585  
 Qy 122 TheProSerLeuSerAlaMetValLeuThrPheValGuaSerValGuaSer 141  
 Db 586 ATCCGATGCGTGGCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 645  
 Qy 142 PhenAlaGluValGluValGluValGluValGluValGluValGluValGlu 161  
 Db 646 TTATACCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 705  
 Qy 162 LeuLeuValValValValValValValValValValValValValValValVal 181  
 Db 706 TGTTCATCATCAAAATACATATGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 765  
 Qy 182 AsnIleThrIleGluValGluValGluValGluValGluValGluValGluVal 201  
 Db 766 AAATACCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 825  
 Qy 202 GlValAlaMetLeuSerAsnIleProGlyAspValGuaSerValGuaSerVal 221  
 Db 826 GGGCGCTGATTTTCTCTCCACGCTGAGATGCTGAGATGCTGAGATGCTGAG 885  
 Qy 222 ValHisThrValAlaThrIleThrValAlaAspGlyValGuaSerValGuaSer 241  
 Db 886 GTTCCAGCTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 945  
 Qy 242 GlAspAspGluValGluValGluValGluValGluValGluValGluValGlu 261  
 Db 946 GGGGAG 1005  
 Qy 262 GlAlaGluThrValValAlaMetLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 281

Db 1006 GGTGACAGCGTTAGAAACACACACACACACACACACACACACACACACAC 1065  
 Qy 282 TyLeuLeuPhePheValThrPheMetGluValValLeuValPheValAspVal 301  
 Db 1066 AACCTCTTTTCTGCTAGCTTATGCGGACAGACATTTTCCAGAGATTAATCA 1125  
 Qy 302 TTTTCTTTTCTGCTAGCTTATGCGGACAGACATTTTCCAGAGATTAATCA 321  
 Db 1126 TACTGATCCGAGTTCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1185  
 Qy 322 ValLeuLeuValLeuGluValGuaSerValGuaSerValGuaSerValGuaSer 341  
 Db 1186 CCGGATGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1245  
 Qy 342 TySerThrIleLeuAlaPheThrIleAspPheSerValGuaSerValGuaSer 361  
 Db 1246 GATCAACGCTATGATGATGAAACACTCTTACGCTCATATGCTATGATGAT 1305  
 Qy 362 TTTTCTTTTCTGCTAGCTTATGCGGACAGACATTTTCCAGAGATTAATCA 381  
 Db 1306 TACTGAG 1365  
 Qy 382 SerGluPheGluValGuaSerValGuaSerValGuaSerValGuaSerVal 401  
 Db 1366 TCGGCTTTTCTGCTAGCTTATGCGGACAGACATTTTCCAGAGATTAATCA 1425  
 Qy 402 AsnSerProTrpIleThrValLeuAspValGuaSerValGuaSerValGuaSer 421  
 Db 1426 ATGACCTTGTGAG 1485  
 Qy 422 TySerThrIleLeuAlaPheThrIleAspPheSerValGuaSerValGuaSer 441  
 Db 1486 AATCAG 1545

RESUME 9-877-476-17

; Sequence 17, Application US/0987476

; Patent No. US2002049994A1

; APPLICANT: Jencorski, Jan G.

; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES

; FILE REFERENCE: 07148-108001

; CURRENT APPLICATION NUMBER: US/09-877-476

; PRIOR FILING DATE: 2000-06-08

; SOFTWARE: PatsSeq for Windows Version 4.0

; SEQ ID NO 17

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: INFORMATION: 5' 222 bp from A. thaliana PXL (SEQ ID NO:11) and

; OTHER INFORMATION: NO:3) having a mutation at position 917;

; NAME/KEY: CDS designated AC74 G366; hypothetical.

; LOCATION: (1)...(1515)

US-09-877-476-17

Alignment Scores:

Pred. No.: 2,66e-208

Length: 1518

Percent Similarity: 98.61%

Best Local Similarity: 97.21%

Query Match: 97.21%

Mismatches: 5

Indels: 1

Gaps: 1

DB:

SEQ14-JOIN-SEQ4 (1-432) x US-09-877-476-17 (1-1518)



```

OY 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProlIleuValGValSerVal 21
DB 226 CGGGTAAACCTGGTGAATCATCTACTCTCCACACCCCATCTGATAGATATC 285
OY 22 SerValGluPheLeuValPheValGluValGluValGluValGluValGluVal 31
DB 286 TCGAGCTCATGATATCTTTATCATATGAAAGATCTAT --- CATTCTGGAGAGC 342
OY 42 ThnCysAspAspSerTyrPheLeuValGluValGluValGluValGluValGluVal 61
DB 343 AGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 402
OY 62 GluAspGluThrIleGluProCysIleLeuLeuValPheProAspTyrThrPheAla 81
DB 403 GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 462
OY 82 ALAAlaGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 101
DB 463 GGGGGGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 522
OY 102 PheAlaGluValPheValGluValGluValGluValGluValGluValGluValGluVal 121
DB 523 ACACACCTGTAACCTTAAGATATAGTATCTGTGGTGAACATCAGCATCTTTATATCCA 582
OY 122 TheProSerLeuSerAlaMetValAlaValThrPhePheGluSerAnnValAcSer 141
DB 583 ATCTATATCTCTCCCGGAGAGTGTATACATCTTCAATCTCCACAGCATGTAGAAGC 642
OY 142 PheAlaGluValGluMetGlyCysSerAlaGlyIleAlaIleAlaPheLeuAlaVal 161
DB 643 TTAACTCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 702
OY 162 LeuLeuValIleValIleValThrTyrAlaIleValIleValSerThrGluValIleThrTyr 181
DB 703 TTCTTCTGATGCTAAATATAGTATGCTCTGTGTGGTGAACAGAGACATCATAT 762
OY 182 AsnIleValGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 201
DB 763 ACATCTACCTGTGGATATAGTATCAATAGTATGATGATGATGATGATGATGATGATGAT 822
OY 202 GluValAlaIleLeuLeuSerAnnValPProGluValAspA9AcATGATSerTyrTyrGluLeu 221
DB 823 GGGGGGCTATTTCTCTCCACAGCTGGAGATGTAGACATGCTCCAGTGAAGAGCTTA 882
OY 222 ValIleThrValAlaThrIleThrIleGluValAspGlyValSerPheAspGluValGlu 241
DB 883 GTTACAGCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 942
OY 242 GluAspAspGluMetGlyIleGlyValSerLeuSerTyrAspIleThrAspValAla 261
DB 943 GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1002
OY 262 GluValThrValIleValIleValIleValIleValIleValIleValIleValIleVal 281
DB 1003 GTCTCAGAGCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1062
OY 282 LeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 301
DB 1063 AACACTCTTTTCTGATCTCTATGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1122
OY 302 TyrTyrValProAspPheValLeuAlaIleAlaPheValIleAlaIleAlaIleAlaIle 321
DB 1123 TACTAACTCCGAGTTTCAATCTCTATGAGATATTTATATATAGAGAGAGAGAGAGAGAGAG 1182
OY 322 AlaValIleIleValLeuValSerLeuAlaLeuAlaProIlePheValGluAlaSer 341
DB 1183 GCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1242
OY 342 ArgSerThrLeuAlaGluPheValAnnThrSerSerSerSerSerSerSerSerSerSer 361
DB 1243 AGATCAATGATATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1302

```

```

OY 362 TyrIleGluAlaGlyGlyMetValGlyGlyAnnValGlyValTyrPheIleAlaLeuGly 381
DB 1303 TAAATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1362
OY 382 SerGlyPheValGlyAspSerAlaValAlaTTPAlaIleLeuAnnValAlaPheSerThr 401
DB 1363 TCAGCTTTAGCTATGATAGTGGATGTGGTGGTCTTACATCATCTCAAGCTTCGACA 1422
OY 402 AsnSerProGluGluGluCysIleAlaAspGlyTyrProValIleThrLeuSerAspGly 421
DB 1423 ANATATCTCTGGAGACACTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1482
OY 422 LysSerGluThrValGlyAlaGluValAspGlyValSer 432
DB 1483 AAGTCAGAGACTCTGCTCCACAGAGCTGCTGCTCC 1515
RESULT 10
US-09-877-476-33
Patent No. US20020049994A1
GENERAL INFORMATION:
APPLICANT: Blacklock, Brenda J.
TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
FILE REFERENCE: 07146-108001
CURRENT APPLICATION NUMBER: US/09/877,476
PRIORITY CLAIM: US/00/06-08
PRIORITY CLAIM NUMBER: US 60/210,326
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 36
US-09-877-476-33
SEQ ID NO 33
LENGTH: 1524
ORGANISM: Artificial Sequence
FEATURE INFORMATION: 1524 bp from B. ovis elongase KCS (SEQ ID NO.3)
OTHER INFORMATION: having a mutation at position 920; designated bn
LOCUS: 1524 bp (1518)
US-09-877-476-33
Alignment Scores:
Pred. No.: 2,686-258
Score: 99.91, 50
Matches: Live: 322
Best local Similarity: 97.91%
Query Match: 97.40%
Indels: 1
Gaps: 1
SR014-JOIN-SR004 (1-432) x US-09-877-476-33 (1-1524)
OY 2 ProValTyrLeuValAspTyrSerCysTyrLeuProProlIleuValGValSerVal 21
DB 226 CGGGTAAACCTGGTGAATCATCTACTCTCCACACCCCATCTGATAGATATC 285
OY 22 SerValGluPheLeuValPheValGluValGluValGluValGluValGluVal 41
DB 286 TCGAGCTCATGATATCTTTATCATATGAAAGATCTAT --- CATTCTGGAGAGC 345
OY 42 ThnCysAspAspSerTyrPheLeuValGluValGluValGluValGluValGluVal 61
DB 343 AGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 405
OY 62 GluAspGluThrIleGluProCysIleLeuLeuValPheProAspTyrThrPheAla 81
DB 406 GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
OY 82 ALAAlaGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 101
DB 465 GGGGGGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 525

```







```

Db 1363 GGGCAGCGCTTAAGCTGTACAGCTCCGCTTGGCTGCTTAAACACATGCAACAGCTCG 1422
Oy 401 ThrAenSerProtpdglHicAyleaSerAyleaSerProtpdglHicAyleaSerAyleaSer 420
Db 1423 AAAAAATGCTGGCAAAATGCTGGCAAAATGCTGGCAAAATGCTGGCAAAATGCTGGCAAA 1482
Oy 421 G145Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4 432
Db 1483 GGTATGCTAGAGATGCTGGCTGGCAACGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1518
RESULTS 14
; Sequence 37, Application US/0987476
; Patent No. 0520020049994A1
; APPLICANT: Jaworski, Jan G.
; TITLE OF INVENTION: STAPHYLOCOCCUS 3-KETONACYL COA
; TITLE OF INVENTION: STAPHYLOCOCCUS 3-KETONACYL COA
; PILE REFERENCE: 07148-108001
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,126
; INVENTION DATE: 2001-06-08
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1: 1521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: 5' 762 bp from A. thaliana PAB1 (SEQ ID NO:1) and
; OTHER INFORMATION: 3' 759 bp from B. napus elongase KCS (SEQ ID NO:3)
; OTHER INFORMATION: 1521 bp from a mutation at position 920; designated
; NAME/KEY: CDS
; DESCRIPTION: (1)...(1518)
US-09-877-476-37

```

```

Alignment Scores: 1,518-1,554
Score: 1521
Percent Similarity: 98.1%
Query Match: 1521
Query Mismatch: 8
Query Gap: 0
DB: 0

```

```

SEQ14-JOIN-SEQ4 (1-1521) X US-09-877-476-37 (1-1521)

```

```

Oy 1 AnProvaThyruLeuValAspThrSerCysLeuProPonIsLeuArgValSer 20
Db 221 ATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 282
Oy 21 ValSerLeuValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
Db 281 GCTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 342
Oy 41 G145Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4 462
Db 343 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 402
Oy 61 G145Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4 480
Db 601 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 500
Oy 81 AlaAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 100
Db 461 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 522
Oy 101 AnProvaThyruLeuValAspThrSerCysLeuProPonIsLeuArgValSer 120
Db 521 AAAAAATGCTGGCAAAATGCTGGCAAAATGCTGGCAAAATGCTGGCAAAATGCTGGCAAA 1482

```

```

Oy 121 ProPonIsLeuArgValSerCysLeuProPonIsLeuArgValSer 140
Db 581 CAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 442
Oy 141 SerPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 160
Db 641 AACTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 702
Oy 161 AnProvaThyruLeuValAspThrSerCysLeuProPonIsLeuArgValSer 180
Db 701 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 762
Oy 181 ThyruLeuValAspThrSerCysLeuProPonIsLeuArgValSer 200
Db 761 ATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 822
Oy 201 G145Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4 220
Db 821 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
Oy 241 LeuValAspThrSerCysLeuProPonIsLeuArgValSer 260
Db 881 CAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 942
Oy 261 G145Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4 280
Db 941 CAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1002
Oy 281 G145Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4 300
Db 1001 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1062
Oy 301 HisTyruValProPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 320
Db 1121 CAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1182
Oy 321 ArgAlaValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 340
Db 1181 AACTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1242
Oy 341 SerPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 360
Db 1241 CAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1302
Oy 361 AnProvaThyruLeuValAspThrSerCysLeuProPonIsLeuArgValSer 380
Db 1301 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1362
Oy 381 G145Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4 400
Db 1361 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1422
Oy 401 AnProvaThyruLeuValAspThrSerCysLeuProPonIsLeuArgValSer 420
Db 1421 AACTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1482
Oy 421 G145Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4Join-Seq4 440
Db 1481 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1518
RESULTS 15
; Sequence 31, Application US/0987476
; Patent No. 0520020049994A1
; APPLICANT: Jaworski, Jan G.
; TITLE OF INVENTION: STAPHYLOCOCCUS 3-KETONACYL COA
; TITLE OF INVENTION: STAPHYLOCOCCUS 3-KETONACYL COA

```



GenCode version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 6, 2003, 14:56:55 ; search time 187 seconds

Size: 5202,477 Million cell updates/sec

Title:

Sequence: 1 NPVIVQVSYLPPHRYV8.....PWKIDSGSHETWONRS 432

Scoring table:

Match 10.0, Xmatch 0.5

Gapop 6.0, Gapext 7.0

Delop 6.0, Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

MODE=frame\_plus\_p2n model  
-DB=NCBI  
-LOOPT=1  
-LOOPT=0 -UNITS=bits -STATE=1 -END=1 -MATRIX=blomus2 -TRANS=human40.cdi  
-MODE=LOCAL -OUTPR=p10 -MODE-ext -HAPSIZE=100 -MINLEN=1 -MAXLEN=2000000000  
-USER=MEIWA087476.acn 1\_218.0runat\_06012003.124916.9 -MCPU=6 -ICPE=3  
-WAK=THROU=10 -THREASH=1 -XCA=NO -ICPE=10 -ICPE=10.5 -TGAPOP=6 -TGAPEXT=7  
-TGAPOP=10 -TGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1. /SID82/seqdata/geneseq/emb1/NA1980.DAT.\*  
2. /SID82/seqdata/geneseq/emb1/NA1981.DAT.\*  
3. /SID82/seqdata/geneseq/emb1/NA1982.DAT.\*  
4. /SID82/seqdata/geneseq/emb1/NA1983.DAT.\*  
5. /SID82/seqdata/geneseq/emb1/NA1984.DAT.\*  
6. /SID82/seqdata/geneseq/emb1/NA1985.DAT.\*  
7. /SID82/seqdata/geneseq/emb1/NA1986.DAT.\*  
8. /SID82/seqdata/geneseq/emb1/NA1987.DAT.\*  
9. /SID82/seqdata/geneseq/emb1/NA1988.DAT.\*  
10. /SID82/seqdata/geneseq/emb1/NA1989.DAT.\*  
11. /SID82/seqdata/geneseq/emb1/NA1990.DAT.\*  
12. /SID82/seqdata/geneseq/emb1/NA1991.DAT.\*  
13. /SID82/seqdata/geneseq/emb1/NA1992.DAT.\*  
14. /SID82/seqdata/geneseq/emb1/NA1993.DAT.\*  
15. /SID82/seqdata/geneseq/emb1/NA1994.DAT.\*  
16. /SID82/seqdata/geneseq/emb1/NA1995.DAT.\*  
17. /SID82/seqdata/geneseq/emb1/NA1996.DAT.\*  
18. /SID82/seqdata/geneseq/emb1/NA1997.DAT.\*  
19. /SID82/seqdata/geneseq/emb1/NA1998.DAT.\*  
20. /SID82/seqdata/geneseq/emb1/NA1999.DAT.\*  
21. /SID82/seqdata/geneseq/emb1/NA2000.DAT.\*  
22. /SID82/seqdata/geneseq/emb1/NA2001.DAT.\*  
23. /SID82/seqdata/geneseq/emb1/NA2002.DAT.\*  
24. /SID82/seqdata/geneseq/emb1/NA2003.DAT.\*

Prod. No. is the number of results predicted by chance to have a  
score as high as the best score. The results are printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query	Length	DB	ID	Description
1	2244	99.7	1521	24	AA085506	A. thaliana FAE1-B
2	2244	99.7	1521	24	AA085507	A. thaliana FAE1-B
3	2244	99.6	1521	24	AA085508	A. thaliana FAE1-B
4	2240	99.6	1521	24	AA085507	A. thaliana FAE1-B
5	2237	99.4	1521	24	AA085506	Alternative versio
6	2237	99.4	1521	24	AA085505	A. thaliana FAE1-B
7	2233	99.3	1521	24	AA085509	A. thaliana FAE1-B
8	2188	97.7	1518	24	AA085504	Brassicica napus fat
9	2188	97.7	1518	24	AA085508	Brassicica napus fat
10	2191	95.5	1518	24	AA085508	Brassicica napus fat
11	2191	95.5	1518	24	AA085508	Brassicica napus fat
12	2191	95.5	1518	24	AA085508	Brassicica napus fat
13	2191	95.5	1518	24	AA085508	Brassicica napus fat
14	2191	95.5	1518	24	AA085508	Brassicica napus fat
15	2191	95.5	1518	24	AA085508	Brassicica napus fat
16	2191	95.5	1518	24	AA085508	Brassicica napus fat
17	2182	97.4	1790	32	AF927411	Brassicica napus FAE
18	2181	96.9	1521	24	AA085519	Alternative FAE1-B
19	2181	96.9	1521	24	AA085519	Alternative FAE1-B
20	2160	96.0	1521	24	AA085518	A. thaliana FAE1-B
21	2146.5	95.4	1521	24	AA085515	Brassicica napus eio
22	2143.5	95.3	1736	34	AA085502	Brassicica napus fat
23	2143.5	95.3	1736	34	AA085502	Brassicica napus fat
24	2067	91.9	1521	24	AA085514	Brassicica napus fat
25	2061	91.6	1521	24	AA085517	Brassicica napus fat
26	2018	89.7	1709	34	AA085517	Alternative versio
27	2018	89.7	1709	34	AA085517	Alternative versio
28	2015	89.6	1641	17	AA077036	Arabidopsis thalia
29	2015	89.6	1709	34	AA085500	Arabidopsis fatty
30	2015	89.6	1709	34	AA085500	Arabidopsis fatty
31	2014.5	89.5	1442	16	AA090312	Brassicica secton'wa
32	1985.5	88.2	1442	16	AA090211	Brassicica condensin
33	1985.5	88.2	1442	16	AA090211	Brassicica condensin
34	1654	73.5	4313	34	AA172086	DNA sequencing enzy
35	1524.5	67.8	1611	20	AA083221	A. thaliana E15 DN
36	1524.5	67.8	1611	20	AA083221	A. thaliana E15 DN
37	1508.5	67.0	1548	30	AA083223	Arabidopsis thalia
38	1497.5	66.6	1855	21	AA083776	Arabidopsis thalia
39	1484.5	66.3	1474	20	AA083218	A. thaliana E12 DN
40	1484	66.0	2509	32	AA083219	Arabidopsis thalia
41	1484	66.0	2509	32	AA083219	Arabidopsis thalia
42	1478.5	65.7	1512	20	AA083219	Arabidopsis thalia
43	1466.5	65.2	1704	16	AA090217	Condomination syn
44	1377.5	61.2	2343	22	AA080968	Ketoacyl Acp synth

## ALIGNMENTS

Result	Score	Query	Length	DB	ID	Description
AA085506	standard; DNA; 1521 BP.					
AC	AA085506					
XX	22-WK-2002 (first entry)					
DE	A. thaliana FAE1-B - karyolase KCS chimeric gene, At114 mutant 42.					
DE	Fatty acid elongase - karyolase Ckb synthase, elongase KCS, acryase					
XX	very long chain fatty acid; VLCFA; FAE1 gene; chimeric; mutant; ds					
XX	Chimeric - Arabidopsis thaliana.					
OS	Chimeric - Brassica napus.					
XX	Key					
XX	Location/Qualifiers					
XX	1..1521					

```

FT /tag= a
FT /product= A. thaliana FAE1-Braressia napus elongase KCS
FT 1..342
FT /tag= b
FT /replace (375, A)
FT mutation
FT /tag= c
FT /replace (132, C)
FT /tag= d
FT /replace (132, D)
FT /note= "Braressia napus elongase KCS gene"
XX WC300194555-A2.
PP 13-DEC-2001.
XX 08-JUN-2001; 2001NOV-08181737.
XX 08-JUN-2000; 2001NOV-012069.
XX 08-JUN-2000; 2001NOV-012069.
XX (UHM1.) UNIV.MIAMI.
XX Jaworski JG, Blacklock BJ.
XX WPI; 2002-154572/20.
XX WPI; 2002-154572/20.
XX New fatty acid elongase 3-ketocacyl CoA synthase polypeptide and nucleic
XX acids encoding the polypeptide, useful for producing very long chain
XX fatty acids.
XX Diclonore; Fig 2-7; 139pp; English.
XX The invention relates to fatty acid elongase 3-ketocacyl CoA synthase
XX (KCS) polypeptides with altered substrate specificity and/or catalytic
XX activity. The invention also relates to nucleic acids encoding the
XX polypeptides of the invention are useful for catalysing the condensation
XX of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis
XX of very long chain fatty acids. The invention also relates to the use of
XX long chain fatty acids (VLCFA) and may be used in the development of
XX reagents for various purposes, e.g., immunological reagents to monitor
XX expression of elongase KCS polypeptides or nucleic acid probes or
XX screening of elongase KCS polypeptides or nucleic acid probes or
XX programs. The present sequence is a mutant of Arabidopsis thaliana FAE1-
XX Braressia napus elongase KCS cimeric gene, At14 designated as
XX At14 K34N.
XX
XX Sequence 1521 BP: 412 A; 342 C; 344 G; 423 T; 0 other:
Alignment Scores:
Pref. No.: 6,13e-235 Length: 1521
Score: 224.00 Matches: 431
Score Similarity: 99.77% Mismatches: 1
Best Local Similarity: 99.77% Indels: 0
Query Match: 99.73% Gaps: 0
24
S9214-JOIN-S904 (1-1521)
1 AnProvalinLeuValaAlaThrSerCysTyrLeuProProHisLeuArgValSer 20
223 ATTCGGTATTCCTGGTACTACTCTGTGTACCTCCGCCGCCGATCTCGAGTGT 282
0y 21 ValSerGlyPheLeuPheTyrGlnLeuGlyAlaAlaPheThrSerSerAsn 40
Db 283 GTCTTAAGCTAGATGATATTTCTCCATAGTAGAAGCACTATCTCTCCAGAC 342
0y 41 GlyThrCysAlaPheSerSerTrpLeuAlaPheLeuTyrGlnLeuGlyArgSerGly 60
Db 343 GCAAGTGTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 400
0y 61 LeuGlyAlaPheThrHisLeuGlyArgSerSerSerSerSerSerSerSerSer 80
1483 GGTAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1518

```

```

Db 403 CTAGCGATGAACTCAGCGGCCGCGAGGGGCTCTTCAAGTCTCTCCCGAGAGATTTT 462
0y 81 AlalaAlaArgGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 100
Db 463 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
0y 101 AanthAenValAenProCysAspAsgIleGlyLeuValValAenSerSerMetPheAsn 522
Db 523 AAGCCATCTCTACCTCTAGAGATAGATAGATAGATAGATAGATAGATAGATAGAT 582
0y 121 ProThrProSerSerSerAlaMetValAenThrPheGlyLeuAenSerSerValAs 140
Db 583 CAGCATCTCTCTCGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 642
0y 141 SerPheAsnLeuGlyMetGlyCysSerAlaGlyLeuAlaAlaLeuGlyLeuGly 160
Db 643 AGCTTAAGCTCTCTGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 702
0y 161 AenLeuLeuLeuValHisLeuAenThrTrpAlaLeuValSerThrGluLeuLeuThr 180
Db 703 GACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 762
0y 181 TrpAlaLeuGlyTrpAlaGlyPhePheSerSerMetValSerValCysLeuPheArg 200
Db 763 TATACATCTTACCTGCTGATATAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 822
0y 201 GlyValAlaAlaLeuLeuLeuSerAsnProGlyValAspGlyGlyGlySerGlyG 220
Db 823 GTGGGGCGCTGATTTCTCTCCAGAGCTGAGATCTGAGAGCTGAGAGCTGAGAG 882
0y 221 LeuValHisThrValArgThrHisThrGlyLeuAlaPheGlyLeuPheGlyGly 240
Db 883 CTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 942
0y 241 GlnGlyAspGlyAlaGlnGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 260
Db 943 CAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1002
0y 261 AlAGlyAlaThrGlyAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 280
Db 1003 CTGCTCAGCGCTTAAAGAAACATACAGCTGGCTGCTGCTGCTGCTGCTGCTG 1062
0y 281 GlyGlyLeuLeuPhePheValThrPheGlnGlyGlyGlyGlyGlyGlyGlyGly 300
Db 1063 GAAATATCTCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1122
0y 301 TyrTyrTyrProAlaPhePheLeuAlaAlaAlaAlaAlaAlaAlaAlaAla 320
Db 1123 ATCTACTACTGCGCGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1182
0y 321 ArgAlaValLeuLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 340
Db 1183 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1242
0y 341 SerArgSerThrGluHisAlaPhePheLeuThrSerSerSerSerSerSerSer 360
Db 1243 TCAGATCAAGCTGATGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1302
0y 361 AlGlyTrileuAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 380
Db 1303 GATCATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1362
0y 381 GlySerGlyPheGlyCysAlaSerValaTrpValAlaLeuAlaSerValValVal 400
Db 1363 GGTCTAGAGCTTAAAGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1422
0y 401 ThrSerProTyrGlnHisCysGlyIleAspValTyrProValValValLeuSer 420
Db 1423 ACAATGATCTGGAGACCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1482
0y 421 GlySerGlyThrThrThrValGlnHisGlnValSer 432
1483 GGTAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1518

```







Db 943 CMAAGAGACATGAGACAGCAAGTGGATGATGTTGTCGACAGACATACACGATGTT 1202  
 Qy 261 AAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 280  
 Db 1003 CCGTCGTCGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1062  
 Qy 281 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
 Db 1063 GACGACACTCTTTTCTTCT 1122  
 Qy 301 HSTYTYTYVATPACAPPPHSTY 320  
 Db 1123 CATTCT 1182  
 Qy 321 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 340  
 Db 1183 AGAGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1242  
 Qy 341 SGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
 Db 1243 TCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1302  
 Qy 361 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 380  
 Db 1303 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1362  
 Qy 381 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 400  
 Db 1363 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1422  
 Qy 401 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
 Db 1423 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1482  
 Qy 421 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 440  
 Db 1483 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1542  
 Qy 441 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 460  
 Db 1543 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1602  
 Qy 461 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
 Db 1603 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1662  
 Qy 481 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 500  
 Db 1663 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1722  
 Qy 501 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 520  
 Db 1723 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1782  
 Qy 521 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
 Db 1783 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1842  
 Qy 541 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 560  
 Db 1843 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1902  
 Qy 561 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 580  
 Db 1903 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1962  
 Qy 581 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
 Db 1963 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1992  
 Qy 591 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
 Db 1993 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1992

08-JUN-2000; 2000US-2102EP.  
 (UTM1-) UNIV MIAMI.  
 XX Jwercakl JG, Blacklock BJ;  
 XX WP1: 2001-154572/20.  
 XX P-P89B: A617615.  
 New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic  
 acids encoding the polypeptide, useful for producing very long chain  
 fatty acids.  
 XX Disclosure: Fig 2-8; 139pp; English.  
 The invention relates to fatty acid elongase 3-ketoacyl CoA synthase  
 (KCS), polypeptides with altered substrate specificity and/or catalytic  
 properties, and nucleic acids encoding such polypeptides. Polypeptides of  
 the invention are useful for catalyzing the condensation  
 of cis fatty acyl substrate and malonyl CoA, leading to the synthesis  
 of long chain fatty acids (VLCFA) and may be used in the development of  
 reagents for various purposes, e.g., immunological reagents to monitor  
 the presence of antibodies against KCS, and for the development of  
 primers to monitor abundance of an elongase KCS gene in plant breeding  
 programs. The present sequence is a mutant of Arabidopsis thaliana FAE1.  
 CC Brassica napus elongase KCS chimeric gene, A114 designated as  
 CC A114-9709.  
 XX SQ Sequence 1521 BP; 415 A; 341 C; 342 G; 423 T; 0 other:  
 Alignment Scores:  
 Pred. No.: 1,686-234 Length: 1521  
 Percent Similarity: 99.77% Conservative: 130  
 Best Local Similarity: 99.54% Mismatches: 1  
 Query Match: 99.56% Models: 0  
 Db 223 ANTCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 282  
 SQ14-JOIN-SBQ4 (1-432) x AN028507 (1-1521)  
 Qy 1 AsnProValTyrLeuValAspTyrSerCysTyrLeuProTrpHisLeuArgValSer 20  
 Db 223 ANTCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 282  
 Qy 21 ValSerTyrLeuMetAspLeuPheThrGlnIleValArgAlaMetPheSerSerArg 40  
 Db 283 CTGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 342  
 Qy 41 GlyThrCysAspAspSerSerTyrMetAspPheAspArgTyrIleGlnIleAspSerG 60  
 Db 343 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 402  
 Qy 61 LeuValGlnThrIleGlyProCysTyrLeuLeuValLeuProPheGlyThrPhe 80  
 Db 403 CTACGGCTGAATCTCGGCGCCGACGGCGCTGCTGATGCTCTCCCGAGACTTTT 462  
 Qy 81 AlaAlaIleGluGluThrGlnIleValIleIleValIleIleValLeuIleValLeuPhe 100  
 Db 463 GCG 522  
 Qy 101 AsnThrAsnValProGlyAspLeuPheIleValLeuValMetSerMetPheAsn 120  
 Db 523 AACACAGCTACACCTACAGATAGATGATGATGATGATGATGATGATGATGATGAT 582  
 Qy 121 ProThrProGlnSerAlaAlaMetValThrPheThrPheThrPheThrPheThrPhe 140  
 Db 583 CCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 642  
 Qy 141 SerPheAsnIleValGlyMetGlyCysSerAlaGlyIleValIleIleIlePheIleVal 160  
 Db 643 AGCTTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 702



61 LeuGlyAspGluThrHisLeuIleProGluGlyLeuLeuGluValProProGlySerThrPhe 80  
 493 CMAAGCGAGAAAGCTCAAGCGCGCGAGGGGCGCTCTGAGTCTCCCGCGAGAACATTT 462  
 07 81 AlaAlaLeuArgGluGluGluValIleLeuIleGlyAlaLeuGluValLeuPheLys 100  
 494 CAGGCGGCGGCG 100  
 495 CAGGCGGCGGCG 522  
 101 AsnThrAsnValAsnProGlyAspIleIleValValIleValValValValValValVal 120  
 496 AAC 120  
 523 AAC 582  
 121 ProThrProSerGluSerAlaMetValValValValValValValValValValValVal 140  
 497 CAC 140  
 583 CAC 642  
 07 341 SerPheAlaLeuValGlyMetGlyCysSerAlaGlyIleAlaIleAlaLeuAlaLys 160  
 498 CAC 160  
 643 AGCTTTACCTCTGGCGACGGGCTGTGTAGCTGGCGGCTGTATACACCTGTATACACAG 702  
 07 161 AspLeuLeuLeuValHisLysAsnThrValAlaLeuValSerThrGluAsnIleThr 180  
 499 CAC 180  
 703 CAC 762  
 07 181 TyrAsnIleIleAlaGlyPheAsnLysSerMetValSerMetCysLeuPheAspVal 200  
 500 CAC 200  
 763 TATAC 822  
 201 61 GlnGluAlaValIleLeuLeuSerLeuLysGlyValMetAspAspSerLysGlyGlu 220  
 501 CAC 220  
 823 GGTGGGCGCGCTATTTCTCTCCACACACCGCGAGANTGTAGACGCTCAAGTACGAG 882  
 221 LeuValHisThrValArgThrHisThrGluValAlaSerPheLysSerPheLysGlyValGlu 240  
 502 CAC 240  
 883 CAGTTCTACAGCTCAAGCGCATACCGCGAGCTACGGCGAGCTTTTCTGTCTGGTGGCA 942  
 07 241 GlnGlyAspAspGluAsnGlyLysIleValSerLeuSerLysAspIleThrAspVal 260  
 503 CAC 260  
 943 CAC 1002  
 261 AluGlyArgThrValHisThrLeuValIleAlaThrLeuValProMetIleLeuProLeuSer 280  
 504 CAC 280  
 1003 GGTGCGACAGCTTAGAACAACTACACAGCTGGCTGGCTGTATCTTCGTTACGC 1062  
 281 GlnGluSerLeuPhePheThrPheMetGluGlyValMetPheLysAspIleLys 300  
 505 CAC 300  
 1063 GAGAACCTCTCTTTGGTTACTCTTCGCGAGAACTTTCAGAGTAAATACAA 1122  
 301 311 HisPheValProPhePheLeuAlaIleAspIlePhePhePheIleHisIleGly 320  
 506 CAC 320  
 1123 CATTACTCTCCGGAATTTCAACTCTGTCTATCTACCTTTTATATCATCCGAGAGC 1182  
 321 ArgValValIleLeuGlyLeuGlyValMetValAlaLeuAlaProIleMetValGluAla 340  
 507 CAC 340  
 1183 AAGCGCATCTATGTCTCTACAGAAAGCTACCTTACGACGATCGATGAGGCA 1242  
 341 SerArgSerThrLeuThrAspGluIleAsnThrSerSerSerIleTyrTyrLeu 360  
 508 CAC 360  
 1243 TACATCACTCACTTACATGATTTGGAACACTTCACTACCTCATATGATGATGGTG 1302  
 361 AluSerPheIleGluAlaHisLeuValMetValMetValMetValMetValMetValMet 380  
 509 CAC 380  
 1303 CACATCAATGACCAAGAGGATGAGAGAGATGATGATGATGATGATGATGATGATGATG 1362  
 381 GlnSerPhePheLysCysAsnSerAlaValThrValAlaHisGluAsnValLysAsp 400  
 510 CAC 400  
 1363 GGTGTCATCTATGATGTATGATGTATGATGTATGATGTATGATGTATGATGTATGATGT 1422  
 401 411 ThrAsnSerProTyrLeuHisCysLysLeuAspGlyTyrProValLysIleAspSerAsp 420  
 511 CAC 420  
 1423 ACAAATMTCTGGAGACATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1482  
 421 GlnLysSerGluThrArgValGluGluGluGlyArgSer 432

Db 1483 GGTAGTCCAGAGACCTGTGTCTCCACACCGTGGTC 1518  
 RESULT 6  
 AD28505  
 AD28505 standard; DMR; 1521 BP.  
 XX  
 AC AAD28505;  
 XX  
 DX 22-APR-2002 (first entry)  
 XX  
 DE A. thaliana PAEI-B, napus elongase KCS chimeric gene, At114 mutant v1.  
 DE Fatty acid elongase 3-ketocyl CoA synthase; elongase KCS; enzyme;  
 DE very long chain fatty acid; VLCFA; PAEI gene; chimeric; mutant; da.  
 KW Chimeric - Arabidopsis thaliana.  
 OS Chimeric - Brassica napus.  
 CC  
 Key Location/Qualifiers  
 FT 1..1521  
 FT CDS  
 FT /product="A. thaliana PAEI-B, brassica napus elongase KCS  
 FT chimeric protein, At114 mutant v1"  
 FT /note="Arabidopsis thaliana PAEI gene"  
 FT /misc\_feature  
 FT mutation replace (271..372, CT)  
 FT mutation replace (275, A)  
 FT /misc\_feature  
 FT mutation replace (275, A)  
 FT /note="Brassica napus elongase KCS gene"  
 PN W020019455-A2.  
 XX  
 XX 13-DEC-2001.  
 XX 08-JUN-2001; 2001WO-US18737.  
 PF  
 XX 08-JUN-2000; 2000US-10328P.  
 XX  
 XX (UTM-) UNIV MIMMI.  
 PA Jaworski JN, Blacklock BJ;  
 XX WPT: 3000-154577/20.  
 XX P-2808: ARI7613.  
 XX  
 XX New fatty acid elongase 3-ketocyl CoA synthase polypeptide and nucleic  
 XX acid sequences for the polypeptide, useful for producing very long chain  
 XX fatty acids  
 Disclosure: Fig 2-6; 13ppp; English.  
 XX  
 XX The invention relates to fatty acid elongase 3-ketocyl CoA synthase  
 XX activity and nucleic acid molecules encoding such polypeptides.  
 XX Polypeptides of the invention are useful for catalysing the condensation  
 XX of two fatty acids to form a longer chain fatty acid. The polypeptides  
 XX of the invention are especially useful for producing very  
 XX long chain fatty acids (VLCFA) and may be used in the development of  
 XX transgenic plants. The present sequences are mutant transgenes of the  
 XX expression of elongase KCS polypeptides or nucleic acid probes or  
 XX primers to monitor inheritance of an elongase KCS gene in plant breeding  
 XX programs. The present sequences are mutant transgenes of the  
 XX expression of elongase KCS chimeric gene, At114 designated as  
 CC At114 L91C K92K.  
 CC  
 XX Sequence 1521 BP; 413 A; 341 C; 344 G; 423 T; 0 other;

Alignment Scores:



























GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.  
OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: January 6, 2003, 15:22:35 ; Search time 2415 Seconds  
(without alignments)  
5205.968 Million cell updates/sec

Seq12-JOIN-SBQ4

Perfect score: 2255

Sequence: 1 NPVIVDSYSLPPHCHVRS.....PWKIDSKSEKTHVQNRDS 432

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.3  
Xgapop 10.0, Xgapext 0.3  
Xgapop 6.0, Xgapext 7.0  
Xdelop 6.0, Xdelext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame\_p2n\_model -DB=sw-rlh  
-DB=GenBank -OPR=fastp -SUFFIX=rge -MFWATCH=0.1 -LOOKUP=0 -XGAPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-OUT=seq12-join-seq4.rge -OUTDIR=/ -MODE=LOCAL  
-OUTPRG=10 -NORM=raw -REWRITE=300 -HILINK=0 -MAXLEN=200000000  
-USER=MCLEMA1N087476 -CGN=1 -287 -runa\_66012003\_12416-21 -NCPU=6 -ICPU=3  
-MAX\_TREES=1000000000 -NOCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WAPOP=10 -YGAPEXT=0 -XDELOP=6 -XDELXT=7  
-TANOP=6 -FONEXT=7

Database :

1: gb.ba.\*  
2: gb.htg.\*  
3: gb.pat.\*  
4: gb.ov.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ov.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.pr.\*  
11: gb.sts.\*  
12: gb.ny.\*  
13: gb.un.\*  
14: gb.un.\*  
15: gb.ba.\*  
16: gb.un.\*  
17: gb.un.\*  
18: gb.in.\*  
19: gb.un.\*  
20: gb.un.\*  
21: gb.un.\*  
22: gb.ov.\*  
23: gb.pat.\*  
24: gb.ov.\*  
25: gb.pl.\*  
26: gb.to.\*  
27: gb.un.\*  
28: gb.un.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Score	Query	Length	ID	Description
1	2244	99.5	1321	6	AX358167 Sequence
2	2239	99.5	1321	6	AX358167 Sequence
3	2239	99.5	1321	6	AX358167 Sequence
4	2238	99.2	1321	6	AX358177 Sequence
5	2235	99.1	1321	6	AX358171 Sequence
6	2235	99.1	1321	6	AX358171 Sequence
7	2268	57.9	1518	6	AX358165 Sequence
8	2268	57.9	1518	6	AX358159 Sequence
9	2268	57.9	1518	6	AX358159 Sequence
10	2261	57.6	1518	6	AX358173 Sequence
11	2261	57.6	1518	6	AX358189 Sequence
12	2261	57.6	1518	6	AX358189 Sequence
13	2261	57.6	1518	6	AX358179 Sequence
14	2261	57.6	1704	8	AF274750 Brassica
15	2261	57.6	1785	6	AX127154 Sequence
16	2261	57.6	1785	6	AX127154 Sequence
17	2261	57.6	1790	6	AX383742 Sequence
18	2191	57.2	1521	8	AF490461 Brassica
19	2191	57.2	1521	8	AF490461 Brassica
20	2181	56.7	1524	6	AX473106 Sequence
21	2177	56.6	1521	8	AF490460 Brassica
22	2176	56.5	1521	8	AX358171 Sequence
23	2176	56.5	1521	8	AX358195 Sequence
24	2168	56.2	1521	8	AF490459 Brassica
25	2156	55.6	1521	6	AX358187 Sequence
26	2156	55.6	1521	6	AX358187 Sequence
27	2155	55.5	1521	6	AX358193 Sequence
28	2153	55.5	1736	6	AX358161 Sequence
29	2153	55.5	1736	6	AX358161 Sequence
30	2149	55.3	1521	6	AX358195 Sequence
31	2056	91.2	1321	6	AX358185 Sequence
32	2051	89.4	1521	6	AX358183 Sequence
33	2051	89.4	1521	6	AX358183 Sequence
34	2010	89.1	1521	6	AX473108 Sequence
35	2010	89.1	1709	6	AX358157 Sequence
36	2010	89.1	1709	6	AX358157 Sequence
37	2010	89.1	1709	6	AX358157 Sequence
38	2010	89.1	13502	8	AT41420 Arabidopsis
39	1924	85.2	1542	8	AF490461 Brassica
40	1924	85.2	1542	8	AF490461 Brassica
41	1921	85.2	1392	8	BCY14974 Arabidopsis
42	1909	84.7	1468	8	BCY14974 Arabidopsis
43	1884	83.6	1548	8	AF490459 Brassica
44	1884	83.6	1548	8	AF490459 Brassica
45	1882	83.5	1536	8	AT49A21 Arabidopsis

# ALIGNMENTS

RESULT 1



























Qy 332	AlvavililaspvleudluyamLealAlaLeuAlaProilalepAlaGlAlaSer 341	
Db 1071	GGCGTATGATGCTTAGAGAACCTAGCGCTAGACAGCATGATAGAGCATCA 1130	
Qy 342	AntSerthlreulialataphuclvaphrVSeSerSerSerSerSerSerSer 361	
Db 1131	AGTACACGCTACATAGATATGGAACACTGATCATAGCTATATGATATGATGCA 1190	
Qy 362	TYTTLAClualaylVayVmetVayVayVayVayVayVayVayVayVayVay 381	
Db 1191	TGATACAGAACAAAGAGATGAGAAAGATATATATATATGATGATGATGATGAT 1250	
Qy 382	ScnGlyPheGlySerAlaSerAlaValTrpValAlaLeuAlaSerValAlaSerThr 401	
Db 1251	TTAGGCTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1310	
Qy 402	AsSerProTpeLulHicVayVayVayVayVayVayVayVayVayVayVayVay 421	
Db 1311	AT 1370	
Qy 422	UhrVayVayVayVayVayVayVayVayVayVayVayVayVayVayVayVay 432	
Db 1371	AGTCAGAGACTGTGTCAAAAGCTGTGTCC 1403	
RESULTS 14		
LOCUS	AF274750	linear 30 JUN 2001
DEFINITION	Brassica napus beta-ketacyl-CoA synthase (FAE1.1) mRNA, complete	
VERSION	AF274750.1	GI:14695234
FEATURES	Source	Brassica napus
REFERENCE		
AUTHORS		
TITLE	Functional characterization of beta-ketacyl-CoA synthase genes	
REFERENCE		
AUTHORS		
JOURNAL		
MEDLINE		
ABSTRACT		
FEATURES		

AGRTYKKNATGLPLILSEKLLFFVTKKFLKFKIKHYVPKFLADHCTHA	4.75e-194	Length: 1704		
GGAGVYCKKALADTPMSSTVHFGFSTSSISITELATIAKGMKKKNW	2201.50	Matches: 423		
CGAGVYCKKALADTPMSSTVHFGFSTSSISITELATIAKGMKKKNW	98.144	Mismatches: 4		
CGAGVYCKKALADTPMSSTVHFGFSTSSISITELATIAKGMKKKNW	97.638	Indels: 1		
CGAGVYCKKALADTPMSSTVHFGFSTSSISITELATIAKGMKKKNW	6	Gaps: 1		
BASE COUNT	478 a	368 c	371 g	487 t
ORIGIN				
Alignment Scores:				
Pred. No.:				
Score:				
Best Local Similarity:				
Query Match:				
SeqID: JOIN-S604 (1-432) x AF274750 (1-1704)				
Qy 2	ProValTrpValVayVayVayVayVayVayVayVayVayVayVayVayVay 21			
Db 329	CGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 288			
Qy 22	SerGlyVayVayVayVayVayVayVayVayVayVayVayVayVayVayVay 41			
Db 289	TGCGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 345			
Qy 42	ThrProSerLeuSerThrPheUaspPheUaspPheUaspPheUaspPheUasp 61			
Db 346	ACGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 405			
Qy 62	AlaPheUaspPheUaspPheUaspPheUaspPheUaspPheUaspPheUasp 81			
Db 406	CGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 465			
Qy 82	AlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 101			
Db 466	CGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 525			
Qy 102	ThrProSerLeuSerThrPheUaspPheUaspPheUaspPheUaspPheUasp 721			
Db 526	ACGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 585			
Qy 122	ThrProSerLeuSerThrPheUaspPheUaspPheUaspPheUaspPheUasp 141			
Db 586	ACGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 645			
Qy 142	PheUaspPheUaspPheUaspPheUaspPheUaspPheUaspPheUasp 161			
Db 646	TTAGGCTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 705			
Qy 162	LeuLeuValHisValHisValHisValHisValHisValHisValHisValHis 181			
Db 706	TTAGGCTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 765			
Qy 182	LeuLeuValHisValHisValHisValHisValHisValHisValHisValHis 201			
Db 766	ACATATAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 825			
Qy 202	GlyAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 221			
Db 826	GGGCGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 885			
Qy 222	ValHisValHisValHisValHisValHisValHisValHisValHisValHis 241			
Db 886	GTTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 945			
Qy 242	GlyAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 261			
Db 946	GGGCGCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1005			
Qy 262	GlyAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 281			
Db 1006	GTTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1065			
Qy 282	ValHisValHisValHisValHisValHisValHisValHisValHisValHis 301			

[illegible]















Db 1174 AGAGCGTATTGATGAGTGGAGAGATCTCTACTCTACCTGAGCTGGAGCT 1233  
 Qy 341 SerAsgSerThrLeuLanAspGlyIleAsnThrSerSerSerSerIleTyrGluLeu 360  
 Db 1234 TAAAGAGATCAATACAGAGTCTGGTATACCTCTTCAGAGCTCAATTCGTAGAGTGG 1293  
 Qy 361 AlaThrIleGluAlaValGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 380  
 Db 1294 GCTTATACAG 1353  
 Qy 381 GlyGlyGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 400  
 Db 1354 GGTGAGAGTATTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1413  
 Qy 401 ThrAAsnSerProTyrGluLysCysIleAspGlyTyrProValIleTyrLysIleSerAsp 419  
 Db 1414 ACATATATCTCTGGAG 1470  
 RESULT 6  
 : Sequence 5: Application US/0868373  
 : Patent No. 6307128  
 : GENERAL INFORMATION:  
 : APPLICANT: Gen. G.  
 : APPLICANT: Post-Beltemiller, Martha A.  
 : APPLICANT: Todd, James  
 : FILE REFERENCE: 07/148/064001  
 : CURRENT APPLICATION NUMBER: US/08/868.373  
 : NUMBER OF SEQ IDS: 22  
 : SOFTWARE: FASTSEQ for Windows Version 3.0  
 : SEQ ID NO 5: 1512  
 : TYPE: DNA  
 : ORGANISM: Arabidopsis thaliana  
 : US-08-868-373-5

Alignment Scores: 6,186-163 Length: 1512  
 No. gaps: 147/50 Matches: 279  
 Score: 279  
 Percent Similarity: 81.73% Conservative: 61  
 Best Local Similarity: 67.07% Mismatches: 73  
 Diffs Match: 45-141 Gaps: 2  
 SEQ12-JOIN-SHOW (1-132) x US-08-868-373-5 (1-1512)  
 Qy 2 ProValIleValAspTyrSerCysTyrIleProFroProIleCysKysGluSerVal 21  
 Db 271 CCGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 330  
 Qy 22 SerGlyValMetAspIlePheTyrGlnIleGlyGlyGlyGlyGlyGlyGlyGlyGly 390  
 Db 331 CAAAGCTATGAG 450  
 Qy 42 ThrCysAlaGlySerSerTyrPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 61  
 Db 391 GAG 444  
 Qy 62 GlyAlaValIleThrGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 81  
 Db 445 GTCAG 504  
 Qy 82 AlaAlaGlyGluIleThrGluGluGluGluGluGluGluGluGluGluGluGluGlu 101  
 Db 505 GTCCTATGAG 564  
 Qy 102 ThrAsnValAsnProGlyAspIleGlyIleValIleValIleValIleValIleVal 121  
 Db 565 AGCGTGTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 624  
 Qy 122 ThrProSerLeuSerAlaMetValIleAsnThrPheLeuGlySerValAsnValSer 141

Db 625 ACTCAATCATCTCCCTCATCTGATGAGAGATCTCAAGCTAGAGACATCATAGAGT 684  
 Qy 142 PheGluGluGlyIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 161  
 Db 685 TGTAACTATGAG 744  
 Qy 162 LeuLeuIleValIleValIleValIleValIleValIleValIleValIleValIle 181  
 Db 745 TCTATGAG 804  
 Qy 182 AnctIleTyrAlaGlyIleAspAlaGlySerMetValSerAlaCysLeuPheGlyVal 201  
 Db 805 AGCTTATGAG 864  
 Qy 202 GlyAlaAlaIleLeuLeuSerAlaGlyProGlyIleAspGlyGlyGlyGlyGlyGly 221  
 Db 865 GTCCTATGAG 924  
 Qy 222 ValIleThrValIleThrIleThrIleThrIleThrIleThrIleThrIleThrIle 241  
 Db 925 GTCCTATGAG 984  
 Qy 242 GlyAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 261  
 Db 985 GAG 1044  
 Qy 262 GlyThrThrValIleValIleValIleValIleValIleValIleValIleValIle 281  
 Db 1045 CGAG 1104  
 Qy 282 LysLeuLeuPhePheValIleThrPheMetGlyIleValIleValIleValIleVal 301  
 Db 1105 AGCTTATGAG 1164  
 Qy 302 TyrTyrValProGlyPheGlyLeuAlaIleAspIlePheCysIleAlaGlyIleGly 321  
 Db 1165 --TATACAG 1221  
 Qy 322 AlaValIleAspValLeuIleValIleValIleValIleValIleValIleValIleVal 341  
 Db 1222 GTCCTATGAG 1281  
 Qy 342 LysSerThrIleGluAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 361  
 Db 1282 AG 1341  
 Qy 362 TyrIleGluAlaValGlyIleValIleValIleValIleValIleValIleValIle 381  
 Db 1342 ATGAG 1401  
 Qy 382 SerGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 401  
 Db 1402 TCGAG 1461  
 Qy 402 AnctSerProTyrGluIleCysIleAspGlyTyrProValIleValIleValIle 419  
 Db 1462 AG 1509  
 RESULT 6  
 : Sequence 11: Application US/0865299  
 : Patent No. 545947  
 : GENERAL INFORMATION:  
 : APPLICANT: James George Metz  
 : APPLICANT: Kathryn Dennis Lardisabal  
 : APPLICANT: Michael J. Lasser  
 : TITLE OF INVENTION: O-Acyl Transfers  
 : NUMBER OF SEQUENCES: 12  
 : GENE: CYP11B  
 : ADDRESS: Calgene, Inc.  
 : STREET: 1920 Fifth Street



















Alignment Scores:

Read No.: 142e-137 Length: 1733  
Percent Identity: 75.00 Matches: 444  
Percent Similarity: 75.00 Mismatches: 92  
Best Local Similarity: 58.65  
Query Match: 55.794  
Dn: 4  
Gap: 4

SR012-JOIN-SR04 (1-137) x US-08-926-522-21 (1-1733)

Qy 3 ValTyLeuValAlapPyrSerCyfyrLeuProProphicLacysArvalSerValSer 22  
Db 366 GTCTATCTGTGGATCTTGTGATCTATAGCTCCACCGACCTCTATCTGACGAG 118

Qy 23 LysValMetAlapLePherydLelkylValAlapPherSerSerAsnolYthr 42  
Db 429 ATGTCATG-----GACCGACCTCCGGCCGGGGCT 461

Qy 43 CyAspAspSerSerPheLeuAspPheLeuVallelIndleLakSerGlyLeuGly 62  
Db 463 TTTTCTAAGGAGAT---ATGGTTTGAGAGAGATCTTCGAGAGGAGCGGATGGT 518

Qy 63 AGPCTHrHlelcyProGlyLeuGlyValProProtyrHrTherAlaAla 82  
Db 519 GGGAGATCTGCTGCTGATCTGCTGATCTGCTGATCTGCTGCTGCTGCTGCTGCT 578

Qy 83 AlaGlydLthrHrHlelcyVallelIndleLakSerGlyLeuGly 102  
Db 578 GCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 638

Qy 103 AsnValAlapProGlyAspLleLylLeuValAlapSerSerMetPheAsnProThr 122  
Db 639 GCGGCTGACGCGAGCGAGATAGGATATCTGTGCTGCTGCTGCTGCTGCTGCTGCT 698

Qy 123 ProSerLeuSerAlaMetValValAsnThrPheLeuValSerAsnValAspSerPhe 142  
Db 699 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 758

Qy 143 AsnLeuGlyLylMetGlyCySerAlaGlyVallelAlaLeuAspLeuAlaAspLeu 162  
Db 759 ATCTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 818

Qy 163 LeuHleValHis--LysAsnThrTyAlaLeuValSerThrGluAsnLethrTy 181  
Db 819 CTATGCTGTACCTAT 878

Qy 182 AntiLylAlaLylAspAsnSerSerMetValSerAsnLysSerPheLeuValGly 201  
Db 878 ATTTGATCTGTGGCGAATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 938

Qy 209 GlyAlaAlaLylLeuLeuAspAspProGlyLeuAspLeuSerGlyGlyGlyGlyGly 221  
Db 939 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 998

Qy 222 ValHisThrValAspThrHlelcyLylAlaAspLylYlSerPheLysCysValGly 241  
Db 999 CTTCATAGAGTACGCCACAGGCGCTGACGACAGCTGCTGCTGCTGCTGCTGCTGCT 1058

Qy 242 dLysAspAspLysnolYylAllelValSerLeuSerAspLylSerPheValAla 261  
Db 1059 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1118

Qy 262 dLysThrValLysValAsnAlaLthrLeuGlyProLeuLeuLeuSerGly 281  
Db 1119 GGTAGGCGGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1178

Qy 282 LysLeuLeuPheValThrPheMetGlyLysLysLeuPheLysAspLylYlSer 301  
Db 1179 CAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1238

Qy 302 TyTyTyValProMetPheLysLeuAlaLeuAspLylSerHlelAlaLylGlyArg 321  
Db 1238

Search completed: January 6, 2003, 18:58:36

Job time : 62 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_f2n model

Run on: January 6, 2003, 18:10:06 : Search time 49.5 Seconds

Title: SMQ12-JOIN-SEQ4  
Percent score: 2255  
Sequence: 3774.584 Million cell updates/sec  
(without alignments)

Scoring table: B1GSMQ2  
Xgapop 10.0, Xgapext 0.5  
Xgapop 6.0, Xgapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 381593 seqs, 21625194 residues

Total number of hits satisfying chosen parameters: 763186

Minimum db seq length: 0

Maximum db seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: gpr-v11

-D-C/seq12/USFPO.spot/MCZMLXN09877476/runat\_06012003.124918.142/gpr\_query.fasta.1.1166

-D-PublishedApplications\_MA-OPM-fastap -SOPF14-rpb -MINMATCH=0.1

-TRANS-humano.0 -c1 -L124918-142 -M124918-142 -M124918-142

-THE\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=FO -NORM=ext -HEA=SIZE=500 -MINLEN=0

-USING=20000000007476 -C/seq12.1.1.42/runat\_06012003.124918.142 -N989-6 -4500-3

-NO\_XLPLY -NO\_MAP -LARGEQUERY -REL\_SCORES=0 -WAIT -LONGLOG -DEVTIMEOUT=120

-WNN-TIMEOUT=10 -THREASH=1 -XGAPOP=10 -XGAPEXT=0.5 -FONDOP=6 -Fgapext=7

-FONDOP=10 -IGNEXT=0.5 -DELXT=7

Database : PublishedApplications\_MA\*

1: /cgn2\_6/prodata/2/pubseq/US07\_PUBCOM.seq\*

2: /cgn2\_6/prodata/2/pubseq/US06\_PUB.seq\*

3: /cgn2\_6/prodata/2/pubseq/US06\_PUB.seq\*

4: /cgn2\_6/prodata/2/pubseq/US06\_PUBCOM.seq\*

5: /cgn2\_6/prodata/2/pubseq/US06\_PUBCOM.seq\*

6: /cgn2\_6/prodata/2/pubseq/US06\_PUBCOM.seq\*

7: /cgn2\_6/prodata/2/pubseq/US06\_PUBCOM.seq\*

8: /cgn2\_6/prodata/2/pubseq/US06\_PUBCOM.seq\*

9: /cgn2\_6/prodata/2/pubseq/US06\_PUBCOM.seq\*

10: /cgn2\_6/prodata/2/pubseq/US06\_PUBCOM.seq\*

11: /cgn2\_6/prodata/2/pubseq/US06\_PUBCOM.seq\*

12: /cgn2\_6/prodata/2/pubseq/US06\_PUBCOM.seq\*

13: /cgn2\_6/prodata/2/pubseq/US06\_PUBCOM.seq\*

14: /cgn2\_6/prodata/2/pubseq/US06\_PUBCOM.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	2243	99	1521	10	US-09-877-476-13			Sequence 1, Appl
2	2243	99	1521	10	US-09-877-476-13			Sequence 1, Appl
3	2239	99	1521	10	US-09-877-476-13			Sequence 13, Appl

6	2238	99	2	1521	10	US-09-877-476-21		Sequence 21, Appl
7	2232	99	0	1521	10	US-09-877-476-75		Sequence 75, Appl
8	2232	99	0	1521	10	US-09-877-476-75		Sequence 75, Appl
9	2208	97	9	1518	10	US-09-877-476-9		Sequence 9, Appl
10	2208	97	9	1518	10	US-09-877-476-9		Sequence 9, Appl
11	2201	97	6	1518	10	US-09-877-476-17		Sequence 17, Appl
12	2201	97	6	1518	10	US-09-877-476-17		Sequence 17, Appl
13	2201	97	6	1518	10	US-09-877-476-31		Sequence 31, Appl
14	2176	96	5	1521	10	US-09-877-476-25		Sequence 25, Appl
15	2176	96	5	1521	10	US-09-877-476-25		Sequence 25, Appl
16	2156	95	6	1521	10	US-09-877-476-23		Sequence 23, Appl
17	2156	95	6	1521	10	US-09-877-476-23		Sequence 23, Appl
18	2133	95	5	1521	10	US-09-877-476-33		Sequence 33, Appl
19	2133	95	5	1521	10	US-09-877-476-33		Sequence 33, Appl
20	2013	89	3	1521	10	US-09-877-476-41		Sequence 41, Appl
21	2013	89	3	1521	10	US-09-877-476-41		Sequence 41, Appl
22	1519	87	4	1510	10	US-09-877-476-35		Sequence 35, Appl
23	1503	85	6	1510	10	US-09-877-476-35		Sequence 35, Appl
24	1487	85	6	1510	10	US-09-877-476-35		Sequence 35, Appl
25	1487	85	6	1510	10	US-09-877-476-35		Sequence 35, Appl
26	1273	66	5	1479	10	US-09-883-397-13		Sequence 13, Appl
27	1259	55	9	1491	10	US-09-883-397-3		Sequence 3, Appl
28	1259	55	9	1491	10	US-09-883-397-3		Sequence 3, Appl
29	1259	55	9	1491	10	US-09-883-397-3		Sequence 3, Appl
30	1259	55	9	1491	10	US-09-883-397-3		Sequence 3, Appl
31	1259	55	9	1491	10	US-09-883-397-3		Sequence 3, Appl
32	1251	55	9	1491	10	US-09-883-397-3		Sequence 3, Appl
33	1241	55	1	1563	9	US-09-938-842A-1552		Sequence 1552, Appl
34	1235	54	8	1587	9	US-09-938-842A-1598		Sequence 1598, Appl
35	1119	49	6	1550	10	US-09-983-457-7		Sequence 457, Appl
36	1059	47	0	2782	10	US-09-906-457-1		Sequence 1, Appl
37	8302	22	3	1460	10	US-09-938-842A-1587		Sequence 1587, Appl
38	8302	22	3	1460	10	US-09-938-842A-1587		Sequence 1587, Appl
39	483	21	4	811	10	US-09-770-445-774		Sequence 774, Appl
40	483	21	4	811	10	US-09-770-445-774		Sequence 774, Appl
41	370	18	6	1039	10	US-09-878-74-4051		Sequence 4051, Appl
42	370	18	6	1039	10	US-09-878-74-4051		Sequence 4051, Appl
43	270	15	0	276	10	US-09-878-74-14488		Sequence 14488, Appl
44	216	9	6	3443	30	US-09-878-74-2604		Sequence 2604, Appl
45	183	8	1	3114	9	US-10-037-598-35		Sequence 35, Appl

## ALIGNMENTS

RESULT 1  
DB ID: 446-11  
Sequence 11, Application US/09877476  
Patent No. US200204999441  
GENERAL INFORMATION: Jan G.  
APPLICANT: Blacklock, Brenda J.  
TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA  
SYNTHASE-RELATED POLYPEPTIDES  
FILE REFERENCE: 07148-108003  
CURRENT APPLICATION NUMBER: US/09/877,476  
PUBLISHING DATE: 2002-05-08  
PRIOR APPLICATION NUMBER: 07/148-108003  
PRIORITY DATE: 2000-06-08  
PRIORITY FILING DATE: 2000-06-08  
NUMBER OF SEQ ID NOS: 56  
SEQUENCE LENGTH: 1521  
SEQ ID NO 11  
LENGTH: 1521  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: 5' 342 bp from A. thaliana PAIL (SEQ ID NO:1) and  
OTHER INFORMATION: (S80) 3' 342 bp from A. thaliana PAIL (SEQ ID NO:1) and  
OTHER INFORMATION: (N0:3) having mutations at positions 271, 272 and  
OTHER INFORMATION: 275; designated At14g193K928  
LOCATION: (1) ...((1518))





```

Db 583 CAACTCCATCCGCTCCGATGCTGTACACGCTTTCAGCTCCACGACAGTGA 640
Db 584 SerPheAsnGluGlyGlyMetCysSerSerSerSerSerSerSerSerSer 160
Db 585 SerPheAsnGluGlyGlyMetCysSerSerSerSerSerSerSerSerSer 160
Db 613 AGCTTTAACTGCTGGATCGGCTGTAGTCCGCTGTATACGCTATCTCCGAC 702
Db 614 AGCTTTAACTGCTGGATCGGCTGTAGTCCGCTGTATACGCTATCTCCGAC 702
Db 161 AATLLeuLeuLeuValHisValAsnThrValLeuLeuValSerThrGluAsnIlePhe 180
Db 162 AATLLeuLeuLeuValHisValAsnThrValLeuLeuValSerThrGluAsnIlePhe 180
Db 703 GACTTCTGCTGCTACCAAAATATGATGCTCTGTGTGAGCAAGCAATCACT 762
Db 704 GACTTCTGCTGCTACCAAAATATGATGCTCTGTGTGAGCAAGCAATCACT 762
Db 181 TyrAsnIleTyrAlaValAsnAsnGlySerMetMetMetSerCysLeuPheVal 200
Db 182 TyrAsnIleTyrAlaValAsnAsnGlySerMetMetMetSerCysLeuPheVal 200
Db 763 TATACGCTTTACCTGGTGTATAGTCTCCGCTGATGCTGCTGCTGCTGCT 822
Db 764 TATACGCTTTACCTGGTGTATAGTCTCCGCTGATGCTGCTGCTGCTGCT 822
Db 201 GTCATGATGATATLeuLeuSerAsnIleProGlyAsnGlySerSerIleTyrGlu 220
Db 202 GTCATGATGATATLeuLeuSerAsnIleProGlyAsnGlySerSerIleTyrGlu 220
Db 823 GGTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
Db 824 GGTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
Db 221 LeuLeuHisThrValAlaGlnPheHisThrGluAlaGlnPheHisThrGlu 240
Db 222 LeuLeuHisThrValAlaGlnPheHisThrGluAlaGlnPheHisThrGlu 240
Db 883 CAGTGCACACGCTGTACGACGCTATACGCGGCTACGCGGCTGTCTGCTGCTGCA 942
Db 884 CAGTGCACACGCTGTACGACGCTATACGCGGCTACGCGGCTGTCTGCTGCTGCA 942
Db 241 GTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 260
Db 242 GTCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 260
Db 943 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1002
Db 944 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1002
Db 261 AAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 280
Db 262 AAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 280
Db 1003 GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1062
Db 1004 GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1062
Db 1065 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1122
Db 1066 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1122
Db 301 HSTYTYTVALProAspPheValAlaIleGlnPheHisThrGluAlaGlnPhe 320
Db 302 HSTYTYTVALProAspPheValAlaIleGlnPheHisThrGluAlaGlnPhe 320
Db 1123 CATATGAGTCCGCTGATTAACCTTCTATGCTATGCTATGCTATGCTATGCTAT 1182
Db 1124 CATATGAGTCCGCTGATTAACCTTCTATGCTATGCTATGCTATGCTATGCTAT 1182
Db 321 AATLLeuLeuLeuValHisValAsnThrValLeuLeuValSerThrGluAsnIlePhe 340
Db 322 AATLLeuLeuLeuValHisValAsnThrValLeuLeuValSerThrGluAsnIlePhe 340
Db 1183 AGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1242
Db 1184 AGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1242
Db 341 SerAspSerThrValLeuLeuValHisValAsnThrValLeuLeuValSerThr 360
Db 342 SerAspSerThrValLeuLeuValHisValAsnThrValLeuLeuValSerThr 360
Db 1243 TATGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1302
Db 1244 TATGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1302
Db 361 AATLLeuLeuLeuValHisValAsnThrValLeuLeuValSerThrGluAsnIlePhe 380
Db 362 AATLLeuLeuLeuValHisValAsnThrValLeuLeuValSerThrGluAsnIlePhe 380
Db 1303 GATCATGAGTCCGCTGATTAACCTTCTATGCTATGCTATGCTATGCTATGCTAT 1362
Db 1304 GATCATGAGTCCGCTGATTAACCTTCTATGCTATGCTATGCTATGCTATGCTAT 1362
Db 400 GlySerGlyPheCysValAsnThrValLeuLeuValSerThrGluAsnIlePhe 420
Db 401 GlySerGlyPheCysValAsnThrValLeuLeuValSerThrGluAsnIlePhe 420
Db 1363 GGTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1422
Db 1364 GGTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1422
Db 401 ThrAsnSerProGlyHisCysValAsnThrValLeuLeuValSerThrGluAsn 420
Db 402 ThrAsnSerProGlyHisCysValAsnThrValLeuLeuValSerThrGluAsn 420
Db 1423 AATATGAGTCCGCTGATTAACCTTCTATGCTATGCTATGCTATGCTATGCTAT 1482
Db 1424 AATATGAGTCCGCTGATTAACCTTCTATGCTATGCTATGCTATGCTATGCTAT 1482
Db 421 GlySerGlyPheCysValAsnThrValLeuLeuValSerThrGluAsnIlePhe 440
Db 422 GlySerGlyPheCysValAsnThrValLeuLeuValSerThrGluAsnIlePhe 440
Db 1483 GGTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1542
Db 1484 GGTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1542

```

## RESULT 4

```

; US-09-877-476-21
; Sequence 21, Application US/09877476
; Date of Invention: 07/14/2001
; GENERAL INFORMATION
; APPLICANT: JAGRELL, JIM G.
; INVENTOR: JAGRELL, JIM G.
; TITLE OF INVENTION: PANTY ACID KINOMASE 3-KETOACYL COA
; FILE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-10800

```

```

; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-05-08
; PRIOR FILING DATE: 2000-06-08
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: SeqScribe
; FILE NAME: seq12-join-seq4.rnpb
; LENGTH: 1521
; TYPE: DNA
; FEATURE:
; OTHER INFORMATION: 5' 342 bp from A. thaliana PAB1 (SEQ ID NO:1) and
; OTHER INFORMATION: 3' 1521 bp from A. thaliana PAB1 (SEQ ID NO:1)
; OTHER INFORMATION: NO:31 having mutations at positions 275 and 920;
; OTHER INFORMATION: designated At114 K92R G307D; hypothetical
; NAME: YKT3
; NAME: YKT3
; US-09-877-476-21 .....(1518)
;
; Alignment Scores:
; Pred. No.: 9,83e+263 Length: 1521
; Score: 2238.00 Matches: 430
; Score Similarity: 99.54 Mismatches: 2
; Best Local Similarity: 99.54 Mismatches: 2
; Query Match: 99.25 Indels: 0
; DB: 10 Gaps: 0
;
; ;SEQ12-JOIN-SDQ4 (1-432) x US-09-877-476-21 (1-1521)
;
; Db 1 AATPProValThrLeuLeuValHisValAsnThrValLeuLeuValSerThr 20
; Db 223 AATCCGCTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 282
;
; Db 21 ValSerValValMetAspIlePheValGluIleGlyValAlaGlnPheSerSer 40
;
; Db 283 GTCCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 342
;
; Db 41 GTCCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 402
;
; Db 343 GTCCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 402
;
; Db 41 LeuGlyAspThrHisCysValAsnThrValLeuLeuValSerThrGluAsnIlePhe 480
;
; Db 603 CTAAGGCTGATTAACCTTCTATGCTATGCTATGCTATGCTATGCTATGCTAT 462
;
; Db 41 AATLLeuLeuLeuValHisValAsnThrValLeuLeuValSerThrGluAsnIlePhe 500
;
; Db 463 GGTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 522
;
; Db 101 AATPProValThrLeuLeuValHisValAsnThrValLeuLeuValSerThr 120
;
; Db 523 AATCCGCTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 582
;
; Db 121 ProThrProSerLeuSerAlaMetValLeuLeuValHisValAsnThrValLeu 140
;
; Db 583 CAACTCCATCCGCTCCGATGCTGTACACGCTTTCAGCTCCACGACAGTGA 642
;
; Db 141 SerPheAsnGluGlyGlyMetCysSerSerSerSerSerSerSerSerSer 160
;
; Db 643 AGCTTTAACTGCTGGATCGGCTGTAGTCCGCTGTATACGCTATCTCCGAC 702
;
; Db 161 AATLLeuLeuLeuValHisValAsnThrValLeuLeuValSerThrGluAsnIlePhe 180
;
; Db 703 GACTTCTGCTGCTACCAAAATATGATGCTCTGTGTGAGCAAGCAATCACT 762
;
; Db 181 TyrAsnIleTyrAlaValAsnAsnGlySerMetMetMetSerCysLeuPheVal 200
;
; Db 763 TATACGCTTTACCTGGTGTATAGTCTCCGCTGATGCTGCTGCTGCTGCTGCT 822
;
; Db 201 GTCATGATGATATLeuLeuSerAsnIleProGlyAsnGlySerSerIleTyrGlu 220
;
; Db 823 GGTGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882

```

QY 221 LeuValHisThrValArgHisThrGluAlaLeuGlyCysSerPheAspGlyValGln 340  
 DB 883 CTAGTTCACAGCGTTGGTACACGACAFACGGAGCGTGCACAGCTTTTCTGCTGCTGCA 942  
 QY 241 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 260  
 DB 943 CAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1002  
 QY 261 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 280  
 DB 1003 CAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1062  
 QY 281 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
 DB 1063 CAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1122  
 QY 301 HisThrValProPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 320  
 DB 1123 CATCTACATGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1182  
 QY 321 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 340  
 DB 1183 CAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1242  
 QY 341 SerThrValProPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 360  
 DB 1243 CAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1302  
 QY 361 AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 380  
 DB 1303 CAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1362  
 QY 381 GlySerCysPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 400  
 DB 1363 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1422  
 QY 401 ThrAspSerProPheGluAlaCysLeuAspThrValProPhePhePhePhePhePhePhe 420  
 DB 1423 ACAATATGCTTGGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1482  
 QY 421 GlySerCysPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 440  
 DB 1483 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1548

## RESULT 5

US-09-877-476-15  
 : Sequence 15: Application US/0987476  
 : Application: US/0987476  
 : GENERAL INFORMATION:  
 : APPLICANT: Javorzki, Jan G.  
 : TITLE OF INVENTION: FATY ACID ELONGASE 3-KETOACYL COA  
 : TITLE OF INVENTION: SYNTHASE POLYPEPTIDES  
 : CURRENT PRIORITY: 07148-10800  
 : CURRENT FILING DATE: 2001-06-08  
 : PRIOR APPLICATION NUMBER: US/0210,126  
 : NUMBER OF SEQ IDS: 36  
 : SOFTWARE: FatsSeq for Windows Version 4.0  
 : SEQ LENGTH: 1521  
 : TYPE: DNA  
 : ORGANISM:  
 : OTHER INFORMATION: 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and  
 : OTHER INFORMATION: 3' 1179 bp from B. napus elongase KCS (SEQ ID  
 : OTHER INFORMATION: designated A114 G1077; hypothetical  
 : NAME/KEY: CDS  
 : US-09-877-476-15

Alignment Scores: 2,286-263 Length: 1521  
 Predicted No.: 2235, 0  
 Score: 2235, 0  
 Percent Similarity: 95, 548  
 Query Match: 95, 548  
 Query Mismatch: 53, 114  
 Query Indels: 0  
 DB: 10 Gaps: 0  
 SEQ12-JOIN-SRQ4 (1-4132) x US-09-877-476-15 (1-1521)  
 QY 1 AnthrValAnthrValAnthrValAnthrValAnthrValAnthrValAnthrValAnthrVal 20  
 DB 223 ANTHRVALANTHRVALANTHRVALANTHRVALANTHRVALANTHRVALANTHRVALANTHRVAL 282  
 QY 21 ValSerValGluMetPheGluAlaGluAlaGluAlaGluAlaGluAlaGluAlaGluAla 40  
 DB 215 VALSERVALGLUMETPHEGLUALAGLUALAGLUALAGLUALAGLUALAGLUALAGLUALAGLUAL 46  
 QY 41 GlyThrCysAspPheSerThrPheAspPhePhePhePhePhePhePhePhePhePhePhe 60  
 DB 283 GTCTCTAAAGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 342  
 QY 341 GCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 402  
 DB 403 CAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 462  
 QY 61 LeuAlaAspGluThrGluGlnValIleGlyLeuLeuValLeuLeuValLeuLeuValLeu 80  
 DB 407 CTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 462  
 QY 81 AlaAlaAspGluThrGluGlnValIleGlyLeuLeuValLeuLeuValLeuLeuValLeu 100  
 DB 463 GCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 522  
 QY 101 AnthrValAnthrValAnthrValAnthrValAnthrValAnthrValAnthrValAnthrVal 120  
 DB 523 ANTHRVALANTHRVALANTHRVALANTHRVALANTHRVALANTHRVALANTHRVALANTHRVAL 582  
 QY 121 ProGluProGluSerLeuAlaMetValValAspThrPheValLeuAspThrValLeuArg 140  
 DB 583 CMACTCTCATGCTCTCGGAGCTGCTGTAAACATCTTCAGCTTCGACGACGACGACGACGAC 642  
 QY 141 SerPheAsnLeuGlyGlyMetGlyCysSerAlaGlyValIleLeuLeuLeuLeuLeuLeu 160  
 DB 643 ACCTTTTACCTTGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 702  
 QY 161 AspLeuLeuLeuValHisValSerThrValAlaLeuValValSerThrGluLeuLeuLeu 180  
 DB 703 GACTTGTGCATCTTCTTAAATATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 762  
 QY 181 TyrAsnIleThrAlaGlyAspAsnSerMetMetValSerAsnCysLeuPheAspVal 200  
 DB 765 TTTAACTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 822  
 QY 201 GlyAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 220  
 DB 823 GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882  
 QY 221 LeuValHisThrValAnthrValAnthrValAnthrValAnthrValAnthrValAnthrVal 240  
 DB 883 CTAGTTCACAGCGTTGGTACACGACAFACGGAGCGTGCACAGCTTTTCTGCTGCTGCA 942  
 QY 241 GlyValHisThrValAnthrValAnthrValAnthrValAnthrValAnthrValAnthrVal 260  
 DB 943 CAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1002  
 QY 261 AlaValThrValProPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 280  
 DB 1003 CAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1062  
 QY 281 GlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 300  
 DB 1063 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1122  
 QY 301 HisThrValProPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 320  
 DB 1123 CATCTACATGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1182  
 QY 321 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 340  
 DB 1183 CAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1242





```

: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 1524
: ORGANISM: Brasilia napus
: FEATURE: CDS
: LOCATION: (1) ... (1521)
US-09-877-476-3

Alignment Scores:
Pred. No.: 1524
Score: 2208.30
Matches: 424
Mismatches: 3
Best Local Similarity: 98.38%
Query Match: 97.94%
DB: 10
Gaps: 1

SEQ12-JOIN-SBQ (1-432) x US-09-877-476-3 (1-1524)
Qy 2 ProValThrLeuValAspThrSerCysThrLeuProProCysLeuValSerVal 21
Db 229 CGCGTTTACCTGCTGGTACTGCTGCTCCACCCAGCAATGATGATGATC 288
Qy 22 SerValValMetAspLeuPheGlyLeuValValAspThrSerSerAspGly 41
Db 289 TCGACATCGATGATTTTATATCCGCTGAGAACCAAGCTCTCTCTCTCTCT 345
Qy 42 ThrCysAspSerSerThrPheLeuValGlySerLeuValGlySerCysLeu 61
Db 346 AGTCGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 405
Qy 62 GlyAlaThrHisGlyProGlyLeuLeuValValProProGlySerThrPheAla 81
Db 406 GGTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 465
Qy 82 AlaValAspGlyCysGlyLeuValValLeuValValLeuValValLeuValVal 101
Db 466 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 525
Qy 102 ThrValValValProValAspLeuValValLeuValValValValValValVal 121
Db 526 ACCACGCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATG 185
Qy 132 ThrProSerLeuValMetValValValValValValValValValValValVal 141
Db 586 ATCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 645
Qy 142 PheLeuLeuGlyMetCysSerAlaCysValValValValValValValValVal 161
Db 646 TTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 705
Qy 162 LeuValValValValValValValValValValValValValValValValVal 181
Db 706 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 765
Qy 182 AsnThrThrAlaGlyAspValGlySerMetValValValValValValValVal 201
Db 766 AACATTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 825
Qy 202 GlyAlaValValLeuValSerValValValValValValValValValValVal 221
Db 826 GCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 885
Qy 222 ValHisThrValArgThrHisThrGlyValAspGlySerPheValGlyValGln 241
Db 886 GTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 945
Qy 242 GlyAspGlyValGlyCysLeuValValValValValValValValValValVal 261
Db 946 GGAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1005
Qy 262 GlyValThrValValValValValValValValValValValValValValVal 281

```

```

Db 1006 GTCACACGGTTAGAAATACACACACACACACACACACACACACACACAC 1065
Qy 282 TyrLeuValPhePheValThrPheMetCysValValValValValValValVal 301
Db 1066 AACCTCTCTTTTCTGCTTACTCTGTCGGCAGAACTTTTCAAGATTAATCAACAT 1125
Qy 302 TyrTyValProAspPheValValAlaLeuAspPheCysLeuHisAlaGlyVal 321
Db 1126 TACTAGTCCCGATTCATCACTGATTCACATTTTGTTCATCTCCGAGGACGA 1185
Qy 322 AlaValLeuValLeuValCysValValValValValValValValValValVal 341
Db 1186 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1245
Qy 342 ArgSerThrLeuValAspPheGlyValThrThrSerSerSerSerSerSerSer 361
Db 1246 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1305
Qy 362 ThrGlyGlyValGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 381
Db 1306 TACTAGTACCAAGAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1365
Qy 382 SerGlyValPheCysValSerValValValValValValValValValValVal 401
Db 1366 TCGAGCTTAAAGTGTACAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG 1425
Qy 402 AsnSerProProGlyHisCysValLeuAspThrProValValValValValVal 421
Db 1426 ATATGCTTTGGACACATCTGACATGATCCCGCTCAATATGATTTGATTCAG 1485
Qy 422 ValSerGlyThrArgValGlnAsnGlyValSer 432
Db 1486 AATGACGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1518

RESU2_9_476-17
: Sequence 17, Application US/0987476
: Patent No. US2002049994A1
: APPLICANT: Janssen Pharmaceutica NV
: APPLICANT: Janssen, Jan G.
: TITLE OF INVENTION: FAST AND LONG-TERM STORAGE OF DNA
: FILE REFERENCE: 07148-108001
: CURRENT APPLICATION NUMBER: US/09/877,476
: PRIOR FILING DATE: 2000-06-08
: INVENTOR: Janssen, Jan G.
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 17
: LENGTH: 1518
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: 5' 222 bp from A. thaliana PAB1 (SEQ ID NO:1) and
: OTHER INFORMATION: 3' 1256 bp from B. napus elongase ACS (SEQ ID
: OTHER INFORMATION: NO:3) having a mutation at position 917;
: NAME/KEY: CDS
: LOCATION: (1)....(1513)
US-09-877-476-17

Alignment Scores:
Pred. No.: 2,746-258
Score: 98.38%
Matches: 424
Mismatches: 3
Best Local Similarity: 98.38%
Query Match: 97.94%
DB: 10
Gaps: 1

SEQ12-JOIN-SBQ (1-432) x US-09-877-476-17 (1-1518)

```













```

1 CURRENT APPLICATION NUMBER: US 60/497,476
2 CURRENT FILING DATE: 2001-06-08
3 PRIOR APPLICATION NUMBER: US 60/210,326
4 PRIOR FILING DATE: 2000-06-08
5 CURRENT INVENTOR: J. J. B.
6 SOFTWARE: PARSSEQ For Windows Version 4.0
7
8 SEQ ID NO 37:
9
10 TYPE: DNA
11
12 ORGANISM: Artificial Sequence
13
14 OTHER INFORMATION: 5' 762 bp from A. thaliana PAIL (SEQ ID NO:1) and
15 OTHER INFORMATION: 3' 752 bp from B. napus elongase KCS (SEQ ID NO:3)
16 OTHER INFORMATION: AUG has a mutation at position 520: designated
17 OTHER INFORMATION: A4254 G30791.1, Jp000492.01
18
19 NAME/KEY: CDS
20
21 LOCATION: (1)...(1518)
22
23 US-09-877-476-37

```

```

Alignment Scores: 1,274-2452 Length: 1521
Score: 2155.00 No.: 413
Percent Similarity: 97.24 Matches: 10
Query Match: 95.57% Mismatches: 0
Indels: 0
Gaps: 0

```

SD012-JOIN-SEQ4 (1-432) x US-09-877-476-37 (1-1521)

```

Db 1 AATGCGGATATCTGGTACTACTGTTGGTCTGACCTGACCGACCGATCTCAAGATTAGT 282
Qy 21 ValSerIyVaLMeAspIlePhyTCTGlnLeaGlyVaLAspGpThrSerSerAspAsn 40
Db 283 GTCTCTAAAGTCTGGATATTCTTCCAAATGAAAGAGTGAATCTCTACGGAC 342
Qy 41 GlyThyCysAspSerSerTrpLeuAspPhaLeuArgLysIleGlnLysSerGly 60
Db 343 GTGCGCAATGAGTAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 402
Qy 61 LeuGlyAspGlnIleHLeuIleProGlyLeuLeuGlnIleProGlyLeuLeuIlePhe 80
Db 403 CTAGATGAGAGCTACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 462
Qy 81 AlahalaAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 500
Db 463 GCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 522
Qy 101 AsnThrAsnValAsnProGlyAspIleGlyLeuLeuValAsnSerMetPheAsn 120
Db 523 AACACCAAGGTACCTCTAGAGAGATGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 582
Qy 121 ProThrProSerLeuSerAlaMetValValAsnThrPheLysLeuArgSerAsnValArg 140
Db 583 CAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 642
Qy 141 SerPheLeuGlnGlyIleGlnGlySerAsnIleGlnGlnGlnGlnGlnGlnGlnGlnGln 160
Db 643 AGCTATTATCTAGAGAGATGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 702
Qy 161 AspLeuLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
Db 703 GACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 762
Qy 181 TyrAsnIleGlyAlaGlyAsnAsnSerMetValSerMetValSerMetPheAsnVal 200
Db 763 TATACATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 822
Qy 201 GlyGlyAlaAlaLeuLeuSerAsnIleProGlyAspArgGlnSerSerIleGln 220
Db 823 GTGAGAGAGAGATGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882

```

```

Qy 221 LeuLeuIleThrValAsnThrPheLeuThrGlnAlaAspGlyIleAspGlnPheSerGln 240
Db 883 CTAGTTCACACAAGCTTTGAGAGCATACCGAGACTGTGACAGCATGCTTTGTTGCGTCA 942
Qy 241 GlnGlyAspAspGlnAspGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 260
Db 943 CAGGAGACGATGAGACGCGCAAAATTCGGAGTGAGTTGTTCGAGGACATACCGATGTT 1002
Qy 261 AlnGlyIleValIleValIleValIleValIleValIleValIleValIleValIle 280
Db 1003 GCTGCTGAGCGCTTACAGCAAAACATACAGCTTGTGCTGCTGCTGCTGCTGCTGCT 1062
Qy 281 GlnGlyLeuLeuPhePheValThrMetGlyLysLeuPheLysLeuPheLysLeuLys 300
Db 1063 GAGCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1122
Qy 301 HisTyrIleValProAspPheLysLeuAlaIleAspIlePheCysIleLeuIleGly 320
Db 1123 CATCTATAGCTCCGGATTTCAATGCTTATGACATTTGTATACATCCGAGGAG 1182
Qy 321 ArgAlaValIleLeuPheValLeuGlySerLeuLeuLeuLeuLeuLeuLeuLeuLeu 340
Db 1183 AGAGCGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1242
Qy 341 SerArgSerThrLeuIleIleAspPheGlyAsnThrSerSerSerSerIleTrpGlnLeu 360
Db 1243 TCAGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1302
Qy 361 AlaTyrIleLeuAlaLysLysGlyMetLysGlyLysLeuIleValIleTrpIleLeuLeu 380
Db 1303 GATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1362
Qy 381 GlnGlnGlyIleGlyCysAsnSerIleValTrpValAlaLeuAsnAsnValIleArg 400
Db 1363 GGGTCAAGCTTTAAGTGTACAGATGCACTTGTGGTGGCTCTTAAGACATGCTCAAGCT 422
Qy 401 ThrAsnSerProTrogGlnLysCysIleAspAspGlyTrpGlnValIleLeuSerAsp 420
Db 1423 ACAATAGCTCTGGGACACATCTGACAGCATCCGCGATACCGCGTAAATGATCTGAT 1482
Qy 421 GlyIleSerGlnThrArgValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 432
Db 1483 GGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1518

```

Search completed: January 6, 2003, 20:28:54

Job time : 74.5 secs









```

QY 102 ThAaVlaAnProLyAspIleGlyValLeuValValSerSerMetPhaSerPro 121
Db 344 ACQAATGTTAACCTACAGATATAGTATATCTTGCTGATCATGAGCTGTTATACCA 403
QY 122 TheProSerLeuSerAlaMetValValAaThrPhyLeuLeuSerSerMet 141
Db 404 ATCTCTTGCTGCTGATGATGCTGCTATACATCTTACAGCTCCAGCAAGCTAGAGGC 463
QY 142 PhaeAaLeuValGlyMetGlyCysSerAlaGlyValLeuLeuLeuLeuValSer 161
Db 464 TTTAACTGTGGTATGGTGTATGATGGCGGTATAGCCATGTATGATGCAAGAGC 523
QY 162 LeuLeuValValHisValSerThrThrAlaLeuValValSerThrCuaAnLeuThr 181
Db 524 TTGTTCGATGCTTAAATATAGTATGCTCTGTGTGTGATGACAGAGACATCAT 583
QY 182 AnrIleTyrValAaGlyValAlaAlaGlySerMetValSerAlaLeuPheValGly 201
Db 584 ANNTTATACCTGTGTATATAGTGTATGATGATGATGATGATGATGATGATGAT 643
QY 202 GlyAlaAlaLeuLeuLeuSerAnlyProGlyAspArg 214
Db 644 GGGGCGCGCTTTTGTGCTGACAGCTTACAGATGAGATGAG 681
RESULT 4
LOCUS Zoa maye PC0065910 mRNA sequence. 1496 bp mRNA linear HTC 25-MAY-2002
DEFINITION Zoa maye PC0065910 mRNA sequence.
VERSION 1
AUTHORS Hainey, C. F., Dolan, M., Miao, G. H., Vogel, J. M., Whitlitt, M. S.,
KEYWORDS Zoa maye.
SOURCE Zoa maye.
ORGANISM Zoa maye.
REFERENCE 1 (bases 1 to 1496) Autotrophic, sea.
AUTHORS Hainey, C. F., Dolan, M., Miao, G. H., Vogel, J. M., Whitlitt, M. S.,
TITLE Mease Mapping Project/DuPont Consensus Sequences for Design of
REFERENCE 2 (published 2003)
AUTHORS Coe, S. C.
TITLE Direct Submission
JOURNAL Mammalian Genome, 14(12), 1000-1001, 2003.
FEATURES
source
/organism="Zoa maye"
/db_xref="db:EMBL:633522"
/db_xref="db:GenBank:U000000000"
/clone_lib="Mease Mapping Project/DuPont Consensus
Library"
CDS
ORIGIN
This sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
developed by the National Human Genome Research Institute
overseas addressing of BACs in conjunction with the Mease
Mapping Project.
BASE COUNT 277 a 455 c 503 g 261 t
GATCG
Alignment Scores: 9.56e+10 Length: 1496
Score: 991.50 Matches: 193
Percent Identity: 68.00% Conservative: 62
Query Match: 44.06% Gaps: 20
Db: 11

```

```

SEQ12-JOIN-SBQ4 (1-432) x AT108343 (1-1496)
QY 63 GylValGlyThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 81
Db 1486 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1433
QY 82 AlaAAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 98
Db 1432 ACATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1373
QY 99 PhelYanThrAnValAnProLyAspIleGlyValLeuValValSerSerMet 118
Db 1372 TGCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1313
QY 119 PhaeAaProThrProSerLeuSerAlaMetValValAaThrPhyLeuLeuSer 138
Db 1312 TTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1253
QY 139 ValSerPhaeAnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 158
Db 1252 WCTGTACGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1193
QY 159 AlaYanLeuLeuLeuValValHis - LysAnThrThrThrValLeuValSerThr 178
Db 1192 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1133
QY 178 AlnThrThrThrAnlThrValGlyValAlaGlyValSerMetValSerAnValSer 198
Db 1132 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1073
QY 198 ArgValGlyGlyValAlaAlaLeuLeuLeuSerAnlyProGlyAspArgValSer 218
Db 1072 GCGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1013
QY 218 STYrGlyLeuValHisThrValAlaThrThrThrThrValAlaAlaGlyValSer 238
Db 1012 GTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 953
QY 238 AVAlaGlyValAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 258
Db 952 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 893
QY 258 ArgValAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 278
Db 892 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 833
QY 278 GaaSerSerSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 298
Db 832 CTCTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 773
QY 298 a - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 304
Db 772 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 713
QY 304 IPhePhaPhyLeuValAlaLeuAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 324
Db 712 CCGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653
QY 324 AspValLeuLeuAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 344
Db 652 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 593
QY 344 GylValGlyThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 364
Db 592 CTCTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 533
QY 364 ValAlaGlyValThrMetValSerValValValValValValValValValValVal 384
Db 532 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 473
QY 384 AluYanSerAlaValAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 404
Db 472 CAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 413

```



Department of Vegetable Crops, R.W. Melchore Lab  
University of California at Davis (UCD)  
Amundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659















The sequence has been trained to remove vector sequence and contains a minimum of 100 bases of paired value 40 or more. For details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wang R, Kleinhofs A, Wise S (2001) Genetically and physically anchored EST resources for barley genomics. *Barley Genetics Newsletter* 31:29-30. <http://wheat.pw.usda.gov/genpages/ban/31/cover.html>.

BASE COUNT	200 a	223 c	260 g	182 t	2 others
------------	-------	-------	-------	-------	----------

Alignment Scores:

Alignment scores:		
Pred. No.:	3,258-95	Length:
Score:	871.50	Matches:
Percent Similarity:	80.36%	Conservative:
Best Local Similarity:	68.30%	Mismatches:
Query Match:	38.65%	Indels:
DB:	13	Gaps:
		1

SF012-JOIN-SFO4 (1-432) X BT949576 (1-867)

[illegible]



GenStore version 5.1.3  
Copyright (c) 1995 - 2003 CompuGen Ltd.

OK protein - nucleic search, using frame\_plus\_2pn model

Run On: January 6, 2003, 16:29:00 : Search time 1402 Seconds  
Chosen fragments  
6959:735 M11100 cdl1 updates/sec

File: SEQ14-JOIN-SEQ4  
Perfect score: 225  
Sequence: 1 NPPVLYDCEITLPPHKLKVS.....PWKIDSGKSTFVONRS 432

Scoring table: BLOSUM62

Xsmap 10.0, Xsmap 0.5  
Ysmap 10.0, Ysmap 0.5  
Zsmap 10.0, Zsmap 0.5  
Dalign 6.0, Dalign 7.0

Searched: 16154666 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32008132

Minimum Db seq length: 0

Maximum Db seq length: 2000000000

Post-processing: Minimum Match 98

Listing first 45 summaries

Command line parameters:

-MODE=frame\_plus\_2pn model  
-DB=seq14-join-seq4  
-DB-SEQ\_QUERY\_FASTAP\_SUFFIX=rst MINMATCH=0.1 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40 cdl -LIST=45  
-CUTOFF=plc -NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USDB=MCELMAN0897476\_R020\_L1\_1573\_rnaut\_0601009\_1\_24916\_33 -NFP=6 -ICP=3  
-HAPR\_TMPOUT=10 -THREADS=1 -XGAP=10 -XGAPEXT=0.5 -YGAP=6 -YGAPEXT=7  
-YGAPO=10 -YGAPEXT=0.5 -DBLOP=6 -DELETE=7

Database :

1: em\_estab1.\*  
2: em\_estab1.\*  
3: em\_estab1.\*  
4: em\_estab1.\*  
5: em\_estab1.\*  
6: em\_estab1.\*  
7: em\_estab1.\*  
8: em\_estab1.\*  
9: em\_estab1.\*  
10: gb\_est2.\*  
11: gb\_hcc.\*  
12: gb\_hcc.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estab1.\*  
16: em\_estab1.\*  
17: gb\_gse.\*  
18: em\_gse\_luv.\*  
19: em\_gse\_luv.\*  
20: em\_gse\_pln.\*  
21: em\_gse\_vrt.\*  
22: em\_gse\_vrt.\*  
23: em\_gse\_mam.\*  
24: em\_gse\_mam.\*  
25: em\_gse\_mam.\*  
26: em\_gse\_pro.\*  
27: em\_gse\_pro.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
C	1	118.5	821	191	11	AT109713		
C	2	116.5	49.6	682	17	BH693376		BH693376 B0152437R
C	3	100.3	44.6	682	17	BH46730		BH46730 B014157F
C	4	98.5	43.7	915	14	B051080		B051080 EST517495
C	5	98.2	43.7	915	14	B051080		B051080 EST517495
C	6	96.6	41.6	765	14	B098474		B098474 G071W08.
C	7	96.6	41.6	765	14	B098474		B098474 G071W08.
C	8	92.1	41.0	738	12	B058676		B058676 EST48444
C	9	91.5	40.7	755	14	B092186		B092186 G013006.
C	10	91.5	40.7	755	14	B092186		B092186 G013006.
C	11	88.8	39.5	715	13	B058781		B058781 EST40663
C	12	88.4	39.3	800	12	B064966		B064966 EST408585
C	13	87.2	39.0	765	13	B095210		B095210 CA_EB003
C	14	87.2	39.0	765	13	B095210		B095210 CA_EB003
C	15	87.1	38.7	867	13	B194576		B194576 HVN01001
C	16	86.7	38.7	858	12	B044087		B044087 CA_EB002
C	17	86.7	38.7	858	12	B044087		B044087 CA_EB002
C	18	84.9	37.6	830	10	B0642615		B0642615 Cr12_5_11
C	19	84.7	37.6	832	12	B083772		B083772 Zml0_05c0
C	20	81.5	36.0	671	13	B28418		B28418 B1281418
C	21	81.4	36.6	725	14	B012426		B012426 G01108_5_V
C	22	81.0	35.9	864	13	B044393		B044393 CA_EB002
C	23	80.8	35.9	864	13	B044393		B044393 CA_EB002
C	24	80.8	35.9	864	13	B044393		B044393 CA_EB002
C	25	80.4	35.8	665	17	B050982		B050982 AL505481
C	26	79.1	35.2	665	17	B050982		B050982 AL505481
C	27	79.1	35.2	665	17	B050982		B050982 AL505481
C	28	79.0	35.1	662	14	B082310		B082310 G0817423
C	29	78.5	34.9	711	14	B0943166		B0943166 G0716008
C	30	78.5	34.9	711	14	B0943166		B0943166 G0716008
C	31	78.1	34.7	680	14	B047349		B047349 CA_EB001
C	32	76.9	34.2	659	12	B044569		B044569 CA_EB001
C	33	76.9	34.2	659	12	B044569		B044569 CA_EB001
C	34	76.3	33.9	768	13	B143568		B143568 EST337359
C	35	76.3	33.9	768	13	B143568		B143568 EST337359
C	36	75.5	33.6	685	12	B043505		B043505 CA_EB002
C	37	75.6	33.6	715	12	B0128306		B0128306 EST473952
C	38	75.5	33.6	720	14	B081648		B081648 WH2816_8
C	39	75.5	33.6	720	14	B081648		B081648 WH2816_8
C	40	74.5	33.5	642	13	B120152		B120152 G1202159
C	41	74.5	33.3	753	12	B013587		B013587 EST469233
C	42	74.5	33.3	753	12	B013587		B013587 EST469233
C	43	74.5	33.2	641	12	B042842		B042842 CA_EB001
C	44	74.5	33.1	608	14	B047823		B047823 CA_EB000
C	45	74.5	33.1	608	14	B047823		B047823 CA_EB000

# ALIGNMENTS

RESULT	1
AT109713	
DEFINITION	zee mays C119L1_1 mRNA sequence.
ACCESSION	AT109713
KEYWORDS	HC
SOURCE	zee mays.
ORGANISM	zee mays.
REFERENCE	1. Bases 1-2091
AUTHORS	Arthur, L.W., Banafey, M., Morgante, M. and Tingey, S.V.

RESULT	1
AT109713	
DEFINITION	zee mays C119L1_1 mRNA sequence.
ACCESSION	AT109713
KEYWORDS	HC
SOURCE	zee mays.
ORGANISM	zee mays.
REFERENCE	1. Bases 1-2091
AUTHORS	Arthur, L.W., Banafey, M., Morgante, M. and Tingey, S.V.



















[illegible]

243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
841  
842  
843  
844  
845  
846  
847  
848  
849  
850  
851  
852  
853  
854  
855  
856  
857  
858  
859  
860  
861  
862  
863  
864  
865  
866  
867  
868  
869  
870  
871  
872  
873  
874  
875  
876  
877  
878  
879  
880  
881  
882  
883  
884  
885  
886  
887  
888  
889  
890  
891  
892  
893  
894  
895  
896  
897  
898  
899  
900  
901  
902  
903  
904  
905  
906  
907  
908  
909  
910  
911  
912  
913  
914  
915  
916  
917  
918  
919  
920  
921  
922  
923  
924  
925  
926  
927  
928  
929  
930  
931  
932  
933  
934  
935  
936  
937  
938  
939  
940  
941  
942  
943  
944  
945  
946  
947  
948  
949  
950  
951  
952  
953  
954  
955  
956  
957  
958  
959  
960  
961  
962  
963  
964  
965  
966  
967  
968  
969  
970  
971  
972  
973  
974  
975  
976  
977  
978  
979  
980  
981  
982  
983  
984  
985  
986  
987  
988  
989  
990  
991  
992  
993  
994  
995  
996  
997  
998  
999  
1000

284 LeuPhePheValThrPheMetGlyLysLysLeuPheLysAspLysIleLysHisTyr 303  
424 GCTGTGAAGACAAATCATCACCAACTTAGTGCCGTCGGTCTCGCTGCATGCTGATGACCAATC  
484 CTTTTCCTGCCACATTGGTGGGAAGGAGCTATTGAAGCGCAAGATAAGGCT--TAT 540  
304 ValProAspPheLysLeuAlaIleAspHisPheCysteineHisAlaGlyArgAlaVal 323

[illegible]















```

Db 1483 GGTAGTCGAGAGCTGTCTCTCCAGACGTCGTCTCC 1518
RESULT 2
AD28509
AD28509
AD28509 standard; DNA; 1521 BP.
AC AD28509;
22-APR-2002 (first entry)
Xs A. thaliana FAE1-B, napus elongase KCS chimeric gene, At114 mutant #4.
Xs Fatty acid elongase 3-ketocyl CoA synthase; elongase KCS; enzyme;
Xs very long chain fatty acid; VLCFA; FAE1 gene; chimeric; mutant; db.
Xs Chimeric - Arabidopsis thaliana.
Xs Chimeric - Brassica napus.
Xs Key Location/Qualifiers
Xs CDS 1..1521
Xs /product= "A. thaliana FAE1-Brassica napus elongase KCS
Xs chimeric protein, At114 mutant #4"
Xs /tag= a
Xs misc_feature 171..272; C1)
Xs mutation /tag= b
Xs mutation /tag= c
Xs mutation /tag= d
Xs mutation /tag= e
Xs mutation /tag= f
Xs misc_feature 343..1521
Xs Note= "Brassica napus elongase KCS gene"
Xs /tag= f
Xs W0200314655-A2.
13-DEC-2001.
Xs 08-JUN-2001. 2001NC-0818737.
Xs 08-JUN-2000. 2000US-210326P.
Xs (PMF-1) UNIV MIAMI.
Xs Jaworski JC, Blacklock BJ:
Xs NPI. 2002-114572/20.
Xs P-FS08; ARI7617.
Xs New fatty acid elongase 3-ketocyl CoA synthase polypeptide and nucleic
Xs acids encoding the polypeptide, useful for producing very long chain
Xs fatty acids.
Xs Disclosure: Fig 2-10; 13ppr; English.
Xs The invention relates to fatty acid elongase 3-ketocyl CoA synthase
Xs activity and nucleic acid molecules encoding such polypeptides.
Xs polypeptides of the invention are useful for catalysing the condensation
Xs of C20 fatty acyl CoA. They are especially useful for producing very
Xs long chain fatty acids (VLCFA) and may be used in the development of
Xs expression of elongase KCS polypeptides or nucleic acid probes or
Xs primers to monitor inheritance of an elongase KCS gene in plant breeding
Xs schemes. The invention also encompasses a mutant of Arabidopsis thaliana FAE1-
Xs Brassica napus elongase KCS chimeric gene, At114 designated as
Xs Sequence 1521 BP, 415 A, 340 C, 343 G, 423 T; 0 other;

```

```

Alignment Scores: 1.70e-315 Length: 1521
Score: 2245.00 Matches: 430
Percent Similarity: 99.77% Mismatches: 1
Conservative: 1
Non-conservative: 0
Identity: 0
Similarity: 99.77% Indels: 0
Query Match: 25
Gap: 0
DB: 1
SEQ12-JOIN-SEQ4 (1-432) x AD28509 (1-1521)
Qy 1 AtProx1A1rYrLwAlaAaPsrSeSyrYrLdSrOfroProk1ScyAaGValSer 20
Db 223 AtProx1A1rYrLwAlaAaPsrSeSyrYrLdSrOfroProk1ScyAaGValSer 20
Qy 21 ValSerCyAaVwAaWcAaEpLePhyYrCln1aAaYpAaAaPhySerSerVwAa 40
Db 283 QyTCTAGACATGAGTATTCTTACCAATATGAAGAAGCTATCTCTCCAGAAC 42
Qy 41 G1YrH-CyAaPwAaSerSerTlePwAaPheAaVwAaG1a1a1a1a1a1a1a1a1 60
Db 343 QyAGAGTGAATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 102
Qy 61 LeG1AaPwAaH1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1 80
Db 403 TCTAGACATGAGTATTCTTACCAATATGAAGAAGCTATCTCTCTCCAGAAC 142
Qy 81 A1a1A1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1 100
Db 463 SCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Qy 101 AaH1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1 140
Db 523 AtACCACAGCTTAAAGTATAGATATATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 182
Qy 121 ProHrProSerAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 140
Db 583 CACTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 160
Qy 141 SerPheAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 160
Db 643 ACTTAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 182
Qy 161 SerPheAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 180
Db 703 GACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 200
Qy 181 TyAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 220
Db 763 TyAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 240
Qy 201 G1YrH-CyAaPwAaSerSerTlePwAaPheAaVwAaG1a1a1a1a1a1a1a1a1 220
Db 823 GAGTGAATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Qy 221 LeG1AaPwAaH1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1 240
Db 883 CTAGTCAAGGTTTAAAGTATAGATATATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 260
Qy 241 G1YrH-CyAaPwAaSerSerTlePwAaPheAaVwAaG1a1a1a1a1a1a1a1a1 260
Db 943 CAGGAGCAAGCTTAAAGTATAGATATATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 280
Qy 261 A1a1A1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1 280
Db 1003 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
Qy 281 G1YrH-CyAaPwAaSerSerTlePwAaPheAaVwAaG1a1a1a1a1a1a1a1a1 300
Db 1063 GAGGAGCAAGCTTAAAGTATAGATATATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 320
Qy 301 TyAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 320

```











Sequence 1521 BP: 415 A; 341 C; 342 G; 423 T; 0 other;

Alignment Groove:

Alignment Scores:  
 Pred. No.: 1.34e-234  
 Score: 2235.00  
 Percent Similarity: 99.54%  
 Best Local Similarity: 99.31%  
 Query Match: 99.11%  
 na. 24

55012-JOIN-SE04 (1-432) x AAD28507 (1-1521)





























